

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 1, 2002, 06:15:24 ; Search time 121.13 Seconds
(without alignments)
283.778 Million cell updates/sec

Title: US-08-162-407-6
Perfect score: 1242
Sequence: 1 MVLAPAWSPTTYLLLLLLLL.....RPGQVPPVSPQDLILLVH 235

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17.*
1: sp-archaea.*
2: sp-bacteria.*
3: sp-fungi.*
4: sp-human.*
5: sp-invertebrate.*
6: sp-mammal.*
7: sp-mhc.*
8: sp-organelle.*
9: sp-phage.*
10: sp-plant.*
11: sp-rodent.*
12: sp-virus.*
13: sp-invertebrate.*
14: sp-unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	895.5	72.1	294	6 Q9MZV0	Q9MZV0 canis famil
2	894.5	72.0	291	6 Q9MZU9	Q9MZU9 felis silve
3	840	67.6	292	6 Q9GKE0	Q9GKE0 bos taurus
4	746	60.1	274	6 Q9GKD9	Q9GKD9 bos taurus
5	602.5	48.5	172	11 Q81104	Q81104 mus musculus
6	112.5	9.1	579	10 Q9LGG8	Q9LGG8 oryza sativ
7	95.5	7.7	1240	12 Q9DWH8	Q9DWH8 rat cytomeg
8	93.5	7.5	658	10 Q9C570	Q9C570 arabidopsis
9	93	7.5	1217	5 Q17889	Q17889 caenorhabdi
10	92	7.4	251	4 Q9HAD2	Q9HAD2 homo sapien
11	90.5	7.3	5120	13 Q9PU36	Q9PU36 gallus gall
12	89.5	7.2	474	5 Q17610	Q17610 caenorhabdi
13	88.5	7.1	270	4 Q9UMT1	Q9UMT1 homo sapien
14	88.5	7.1	404	10 Q9AWJ4	Q9AWJ4 oryza sativ
15	88.5	7.1	1386	4 Q75064	Q75064 homo sapien
16	88	7.1	250	6 Q9GKE2	Q9GKE2 mus musculus
17	88	7.1	675	11 Q9DBF2	Q9DBF2 mus musculus
18	88	7.1	753	12 Q56971	Q56971 kenedya ye
19	87.5	7.0	470	10 Q9L011	Q9L011 arabidopsis

20	87.5	7.0	946	10 Q22015	O22015 cylindrothe
21	87	7.0	510	5 Q44018	Q44018 leishmania
22	86.5	7.0	299	6 Q9TTT9	Q9TTT9 bos taurus
23	86	6.9	255	11 Q9D3J3	Q9D3J3 mus musculus
24	86	6.9	299	12 Q84647	Q84647 paramacium
25	86	6.9	746	5 Q23600	Q23600 caenorhabdi
26	86	6.9	911	11 Q35407	Q35407 mus musculus
27	85	6.8	282	4 Q9BSAL	Q9BSAL homo sapien
28	85	6.8	289	2 Q9A3K1	Q9A3K1 caulobacter
29	85	6.8	413	11 Q99MM1	Q99MM1 mus musculus
30	85	6.8	1217	4 Q9P2D0	Q9P2D0 homo sapien
31	84.5	6.8	932	11 Q99JH4	Q99JH4 mus musculus
32	84.5	6.8	3726	11 Q61329	Q61329 mus musculus
33	84	6.8	220	4 Q96030	Q96030 homo sapien
34	84	6.8	224	6 Q19031	Q19031 ovis aries
35	84	6.8	263	12 Q36417	Q36417 alcelaphine
36	84	6.8	567	11 Q99J43	Q99J43 mus musculus
37	84	6.8	687	4 Q9H975	Q9H975 homo sapien
38	84	6.8	1234	11 Q9R044	Q9R044 rattus norv
39	84	6.8	1252	11 Q9QXX7	Q9QXX7 rattus norv
40	84	6.8	1252	11 Q9JIX2	Q9JIX2 rattus norv
41	83.5	6.7	199	2 Q9RZL3	Q9RZL3 deinococcus
42	83.5	6.7	290	10 Q9FUH0	Q9FUH0 medicago tr
43	83.5	6.7	524	5 Q9NK88	Q9NK88 drosophila
44	83.5	6.7	530	12 Q07701	Q07701 herpesvirus
45	83.5	6.7	548	5 Q9VJP2	Q9VJP2 drosophila

ALIGNMENTS

RESULT 1

Q9MZV0
ID Q9MZV0 PRELIMINARY: PRT; 294 AA.
AC Q9MZV0;
DT 01-OCT-2000 (TREMREL. 15, Created)
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
DT 01-OCT-2000 (TREMREL. 15, Last annotation update)
DE FLT3 LIGAND.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20358731; PubMed=10902925;
RA Yang S., Sim G.K.;
RT "Molecular cloning of canine and feline flt3 ligand reveals high
RT degree of similarity to the human and mouse homologue but uniquely
RL long cytoplasmic domain."
RL DNA Seq. 11:163-166(2000).
DR EMBL; AF155148; AAF87088.1;
SQ SEQUENCE 294 AA; 32394 MW; 6859917A3B74ABCD CRC64;

Query Match	72.1%	Score 895.5;	DB 6;	Length 294;
Best Local Similarity	77.1%	Pred. No. 6.6e-77;		
Matches 182;	Conservative 12;	Mismatches 35;	Indels 7;	Gaps 3;
QY 1	MTVLAPAWSPTTYLLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDPVTV 60			
Db 1	MIVLAPAWSPTASULLLLLSLPGURGPDCSFHSPISSDFAVKIRELSYLLQDPVTV 60			
QY 61	ASNLQDELGGWRLVLAQRWMLKTVAGSKMGLLRYNTHFVTKCAFQPPSCL 120			
Db 61	ASNLQDELGGWRLVLAQRWMLKTVAGSKMGLLRYNTHFVTKCAFQPPSCL 120			
QY 121	RFVQTNISRLQETSEOLVALKPWITRONFSRCLELQCPDSSTLPPSPRLEATPT 180			
Db 121	RFVQTNISRLQETSEOLVALKPWITRONFSRCLELQCPDSSTLPPSPRLEATPT 180			
QY 181	APQPP-LLLLLLLPGVGLLLAAANCLHW-QTRRTTRPGCEQVPPVPS-----PQD 229			
	: :			

Db 181 APOAPRLLLLLLPPVALLMSTAMWCLHWRRRRRRRRSPYFGEQRTLRPSRSHLPED 236

RESULT 2

Q9MZU9 ID Q9MZU9 PRELIMINARY; PRT; 291 AA.
AC Q9MZU9; DB 6; Length 291;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE FLT3 LIGAND.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20358731; PubMed=10902925;
RA Yang S., Sim G.K.;
RT "Molecular cloning of canine and feline flt3 ligand reveals high
RT degree of similarity to the human and mouse homologue but uniquely
RT long cytoplasmic domain."
RL DNA Seq. 11:163-166(2000).
DR EMBL; AF155149; AAF87089.1; -; 32459 MW; 8F85A10A5EA0DCC6 CRC64;
SQ SEQUENCE 291 AA; 32459 MW; 8F85A10A5EA0DCC6 CRC64;

Query Match 72.0%; Score 894.5; DB 6; Length 291;
Best Local Similarity 80.5%; Pred. No. 8.1e-77;
Matches 178; Conservative 9; Mismatches 33; Indels 1; Gaps 1;

QY 1 MIVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVIV 60
Db 1 MIVLAPAWSPTTSLLLLLLSPGLQTPDCSFHSPISSTFAIKIGKLYLLQDYPVIV 60
QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMOGLLHWRVTEIHFVTKCAFQPPSPCL 120
Db 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMOGLLHWRVTEIHFVTKCAFQPPSPCL 120
QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCCQDSDSTLPPSPRPLEATAP 180
Db 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCCQDSDSTLPPSPRPLEATAP 180
QY 181 APQPP-LLLLLLPVGLLLAAWCLHWRVTEIHFVTKCAFQPPSPGEQ 220
Db 181 APQPP-LLLLLLPVGLLLAAWCLHWRVTEIHFVTKCAFQPPSPGEQ 220

RESULT 3

Q9GKEO ID Q9GKEO PRELIMINARY; PRT; 292 AA.
AC Q9GKEO; DB 6; Length 292;
DT 01-NAR-2001 (TREMBlrel. 16, Created)
DT 01-NAR-2001 (TREMBlrel. 16, Last sequence update)
DE FLT3 LIGAND ISOFORM-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11120823;
RA Wangi W., Brown W.C., Palmer G.H.;
RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain
RT required for receptor binding and function using naturally occurring
RT ligand isoforms."
RL J. Immunol. 165:6966-6974(2000).
DR EMBL; AF282985; AAF9322.1; -; 32390 MW; D68B9ED79221202D CRC64;
SQ SEQUENCE 292 AA; 32390 MW; D68B9ED79221202D CRC64;

Query Match 67.6%; Score 840; DB 6; Length 292;
Best Local Similarity 76.3%; Pred. No. 1.2e-71;
Matches 171; Conservative 12; Mismatches 37; Indels 4; Gaps 2;
QY 1 MIVLAPAWSPTT-YLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 59
Db 1 MIVLAPAWSPTTSLLLLLLSPGLQTPDCSFHSPISSTFAIKIGKLYLLQDYPVT 60
QY 60 VASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMOGLLHWRVTEIHFVTKCAFQPPSPSC 119
Db 61 VASNLQDDKLCGAFWRLVLAQRWMLKTVAGSEKMLLEDVNTFHFVTSKAFQPLPSC 120
QY 120 LRFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCCQDSDSTLPPSPRPLEATAP 179
Db 121 LRFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCCQDSDSTLPPSPRPLEATAP 180
QY 180 TAPQPP-LLLLLLPVGLLLAAWCLHWRVTEIHFVTKCAFQPPSPGEQ 220
Db 181 PGQSPSLLLLLLPPVALLMSTAMWCLHWRVTEIHFVTKCAFQPPSPGEQ 224

RESULT 4

Q9GKD9 ID Q9GKD9 PRELIMINARY; PRT; 274 AA.
AC Q9GKD9; DB 6; Length 274;
DT 01-NAR-2001 (TREMBlrel. 16, Created)
DT 01-NAR-2001 (TREMBlrel. 16, Last sequence update)
DE FLT3 LIGAND ISOFORM-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11120823;
RA Wangi W., Brown W.C., Palmer G.H.;
RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain
RT required for receptor binding and function using naturally occurring
RT ligand isoforms."
RL J. Immunol. 165:6966-6974(2000).
DR EMBL; AF282986; AAF9323.1; -; 30372 MW; 725A7F77A95DA98B CRC64;
SQ SEQUENCE 274 AA; 30372 MW; 725A7F77A95DA98B CRC64;

Query Match 60.1%; Score 746; DB 6; Length 274;
Best Local Similarity 69.6%; Pred. No. 8.6e-63;
Matches 156; Conservative 12; Mismatches 34; Indels 22; Gaps 3;

QY 1 MIVLAPAWSPTT-YLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 59
Db 1 MIVLAPAWSPTTSLLLLLLSPGLQTPDCSFHSPISSTFAIKIGKLYLLQDYPVT 60
QY 60 VASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMOGLLHWRVTEIHFVTKCAFQPPSPSC 119
Db 61 VASNLQDDKLCGAFWRLVLAQRWMLKTVAGSEKMLLEDVNTFHFVTSKAFQPLPSC 114
QY 120 LRFVQTNISRLQETSEQLVALKPWITRONFSRCLELQCCQDSDSTLPPSPRPLEATAP 179
Db 115 -----QDTHQOELKLPWITRONFSRCLELQCCQDSDSTLPPSPRPLEATAP 162
QY 180 TAPQPP-LLLLLLPVGLLLAAWCLHWRVTEIHFVTKCAFQPPSPGEQ 220
Db 163 PGQSPSLLLLLLPPVALLMSTAMWCLHWRVTEIHFVTKCAFQPPSPGEQ 206

RESULT 5

Q61104 ID Q61104 PRELIMINARY; PRT; 172 AA.
AC Q61104;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

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DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE FLT3 LIGAND, T169 FORM.
GN FLT3L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K.,
RA Mattson J., Tsai S., Luh J., Guimares M.J., Mattei M.G., Rosnet O.,
RA Birnbaum D., Hanum C.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U44024; AA93305.1;
DR MGD; MGI:95560; FLT3L.
SQ SEQUENCE 172 AA; 19465 MW; 04F0A010171E3384 CRC64;

Query Match 48.5%; Score 602.5; DB 11; Length 172;
Best Local Similarity 72.6%; Pred. No. 2e-49;
Matches 122; Conservative 15; Mismatches 28; Indels 3; Gaps 2;

Qy 1 MTVLAPANSP-TTYLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 59
Db 1 MTVLAPANSPNSLLLLLSLPCRLGTPDCYFSHSPISSENFVKPRELTHLLKDYPT 60
Qy 60 VASNLQDEELCGGLWRLVLAQRWMLRTVAGSKMGLLRLVTEIHFVTKCAFPQPPSC 119
Db 61 VAVNLQDEKHKALNSLFLAQRWILQKLVAGSKMGLLRLVTEIHFVTSCTFQPLPEC 120
Qy 120 LRFVOTNISRLLQETSEQLVAKPWITR--QNFSCLELQCPQDSSTL 165
Db 121 LRFVOTNISRLLQETSEQLVAKPWITR--QNFSCLELQCPQDSSTL 168

RESULT 6
Q9LGG8 PRELIMINARY; PRT; 579 AA.
AC Q9LGG8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PUTATIVE EXTENSIN-LIKE PROTEIN.
GN P0406H10.6 OR OJ1174_D05.5.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponebare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0406H10."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponebare(GA3) genomic DNA, chromosome 1, BAC
RT clone:OJ1174_D05."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP002524; BAB07956.1;
DR EMBL: AP003118; BAB33013.1;
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR002965; P_rich_extensn.
DR InterPro: IPR000504; RRM.
DR Pfam: PF00560; LRR; 2
DR PRINTS; PR01217; PRICHEXTENS.
DR SMART; SM00370; LRR; 5.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.

SQ SEQUENCE 579 AA; 62607 MW; 04457E18E7405AAF CRC64;

Query Match 9.1%; Score 112.5; DB 10; Length 579;
Best Local Similarity 23.7%; Pred. No. 0.018;
Matches 54; Conservative 28; Mismatches 69; Indels 77; Gaps 11;

Qy 17 LLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRL 76
Db 244 ILLINTGLS-----SCLPPEVGM-LREVTVE-----DVSNRLAGPLPSA 282
Qy 77 VLAQRWMLRTVAGSKMGLLRLVTEIHFVTKCAFPQPPSC 391
Db 283 VAGNRKVEQL-DVAHNLTTGAIPQVCELPRLKNFTFAYNFTTGEPSCAHAVPRYGD 341
Qy 126 NI--SRLLQETSEQLVAKPWITRQNFSSR---CLELQCPQDSSTLPPKSPRLEATAP 179
Db 342 NCLPNRPAQRTLRCAAF-----FARPPVNCARFQCKFFVPALPPSPPPP--SPPP 391
Qy 180 TAPQPPILLLLLPVGLLLAAWCLHWQTRRRTPRPGEQVPPVPS 227
Db 392 PSPPPP-----SPPPSTSPPPSP 411

RESULT 7
Q9DWH8 PRELIMINARY; PRT; 1240 AA.
AC Q9DWH8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE PR2.
GN R2.
OS Rat cytomegalovirus (strain Maastricht).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Muromegalovirus.
OX NCBI_TaxID=79700;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAASTRICHT;
RX MEDLINE=20366325; PubMed=10906222;
RA Vink C., Beuken E., Bruggeman C.A.;
RT "Complete DNA sequence of the rat cytomegalovirus genome."
RL J. Virol. 74:7656-7665(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MAASTRICHT;
RX MEDLINE=20473137; PubMed=11018281;
RA Gruijthuisen Y.K., Beuken E., Bruggeman C.A., Vink C.;
RT "Rat cytomegalovirus R89 is a highly conserved gene which expresses a
RT spliced transcript."
RL Virus Res. 69:119-130(2000).
DR EMBL: AF232689; AAF99111.1;
SQ SEQUENCE 1240 AA; 125612 MW; 33B6C13DC6A272B0 CRC64;

Query Match 7.7%; Score 95.5; DB 12; Length 1240;
Best Local Similarity 33.0%; Pred. No. 1.7;
Matches 29; Conservative 8; Mismatches 18; Indels 33; Gaps 5;

Qy 160 PDSSYL-----PPWSPPR--LEATAPAPQ-PLLLLLLPVGLLLAA 201
Db 1060 FDSSTAVTGEATERTATERPYRPLPGVDLSALPLAPQPTLLSLVPA----- 1112
Qy 202 AWCLHWQTRRRTPRPGEQVPPVPSQD 229
Db 1113 -----QATRASPRPDTAPP-PTPAD 1132

RESULT 8
Q9C5T0 PRELIMINARY; PRT; 658 AA.
AC Q9C5T0;
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01-JUN-2001 (TREMELrel. 17, Created)
 01-JUN-2001 (TREMELrel. 17, Last sequence update)
 01-JUN-2001 (TREMELrel. 17, Last annotation update)
 DE RECEPTOR-LIKE PROTEIN KINASE 4.
 GN ALK4.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Du L., Chen Z.;
 RT "Identification of genes encoding receptor-like protein kinases as
 RT targets of pathogen- and salicylic acid-induced WRKY DNA-binding
 RT proteins";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF224705; AAK28315.1;
 DR InterPro; IPR002902; DUF26.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_kin_actsite.
 DR InterPro; IPR001245; Tyr_kin.
 DR Pfam; PF01657; DUF26; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR SMART; SM00220; S-TRC; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Kinase; Transferrase.
 SQ SEQUENCE 658 AA; 72991 MW; DCF9CF5F1748F614 CRC64;

Query Match 7.5%; Score 93.5; DB 10; Length 658;
 Best Local Similarity 25.8%; Pred. No. 1.3;
 Matches 34; Conservative 16; Mismatches 39; Indels 43; Gaps 6;
 QY 138 LVLPKPTITRONFSRCLEL---QCQPD-----LILLLLLP--VGLLLLAANWCHLWQTRTRTPR--- 172
 DB 195 LVQCTPDLTRODCRCLQVINQIPTDRIGARIINPSCTSRYEIVAFYTESAVPPPP--PP 252
 QY 173 PLEATAPAPQPP-----LILLLLLP--VGLLLLAANWCHLWQTRTRTPR--- 217
 DB 253 PPSITPPVPSAPPSEKEGSKVLVIAIWPVIAVRLFIAGYCFELTRARKSYSTPSAF 312
 QY 218 -GEQVPPVPSQ 228
 DB 313 AGDDITADSLQ 324
 RESULT 9
 ID O17889 PRELIMINARY; PRT; 1217 AA.
 AC O17889;
 DT 01-JAN-1998 (TREMELrel. 05, Created)
 DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
 DE F54F12.1 PROTEIN (EC 3.1.3.48).
 GN F54F12.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barlow K.;
 RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Willow R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
 RA Smailson N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 DR EMBL; Z81548; CAB04464.1;
 DR InterPro; IPR00387; Tyr_phosphatase.
 DR InterPro; IPR00242; Tyr_prot_phptase.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR SMART; SM00194; PTPC; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
 KW Hydrolase.
 SQ SEQUENCE 1217 AA; 135500 MW; 1D1656F460E38508 CRC64;

Query Match 7.5%; Score 93; DB 5; Length 1217;
 Best Local Similarity 23.6%; Pred. No. 2.8;
 Matches 38; Conservative 33; Mismatches 68; Indels 22; Gaps 6;
 QY 83 MERLKTAVGSKMOGL---LERNTEIHFVTKCAFQPPSPCLRFVQTNISRLLOETSEOLV 139
 DB 627 MDAVXAVDGTKYSSVIDALEKISTMDLDQKQKFKAPATLKAMDL-----FFASYASNL 682
 QY 140 ALKPWITRONFSRCLELOQCPDSSTL---PPWSPRPLEATAP-----QPPLLLLL 191
 DB 683 ALRPQPTTSDPTAAAPVPIPNKGLNGNPPSPSPPLPPVASTPAATEESNMLLYII 742
 QY 192 LPVGLLLLLAA-----ANCLHWQTRTRTPRPGQVPPVPS 227
 DB 743 GAVGLLVVAIIIGVLFVFFQKKKKDKPD--PPAPLP 781

RESULT 10
 ID Q9HAD2 PRELIMINARY; PRT; 251 AA.
 AC Q9HAD2;
 DT 01-MAR-2001 (TREMELrel. 16, Created)
 DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMELrel. 17, Last annotation update)
 DE CDNA FLJ11798 FIS, CLONE HEMBA1006198, WEAKLY SIMILAR TO PROLINE-RICH
 DE PROTEIN MP-2 PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=WHOLE EMBRYO, MAINLY HEAD;
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
 RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
 RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
 RA Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y., Oshima A.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK021860; BAB13917.1;
 DR InterPro; IPR002965; P-rich_extensn.
 DR PRINTS; PR01217; PRICHEXTENS.
 SQ SEQUENCE 251 AA; 26607 MW; 420195B27966FD41 CRC64;

Query Match 7.4%; Score 92; DB 4; Length 251;
 Best Local Similarity 31.9%; Pred. No. 0.64;
 Matches 44; Conservative 9; Mismatches 39; Indels 46; Gaps 10;
 QY 115 PPPCLRFVQTNIS-----RLQETSEQVAVLKPTWITRONFSRCLELOQCPDSSTLPPPW 169
 DB 115 PPPCLRFVQTNIS-----RLQETSEQVAVLKPTWITRONFSRCLELOQCPDSSTLPPPW 169

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Query Match          7.3%  Score 90.5;  DB 13;  Length 5120;
Best Local Similarity 24.3%;  pred. No. 22;
Matches 45;  Conservative 19;  Mismatches 72;  Indels 49;  Gaps 7;

QY 90 AGSKMOLLERVRVTEIHF-----VTKAFQPPPPSCLRRVQVN----- 126
    | | | | | : | | | | | : | | | | | : | | | | | :
Db 2224 AARKMSTVTGTGIKIHHEDSHKELSDMTRINTGATSEQPPLCVASVYKPEASETPA 2283
    | | | | | : | | | | | : | | | | | : | | | | | :
QY 127 --ISRLLQTSSE-QLVALKPWITRQNF-----SRCLQLCCQSDSTLPPWPSPRLPEATAP 179
    | | | | | : | | | | | : | | | | | : | | | | | :
Db 2284 VPTPRVVSKTSTVSMPSAPALTSKVSFLRSSLDSPAQSPSPSPSPSPSPSPSPSPSPSP 2343
    | | | | | : | | | | | : | | | | | : | | | | | :
QY 180 TAQP-----PLLLLLLPVGLLLAAAWCLH--WORTRRTRPRGEQV 221
    | | | | | : | | | | | : | | | | | : | | | | | :
Db 2344 ILPKPAIYPKKKSOIQAPMATAPTAVPLVTSVATLESAAVLKNHWPVTKYTTTPT-PPV 2402
    | | | | | : | | | | | : | | | | | : | | | | | :
QY 222 PPVPS 226
    | | | | |

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Db      2403 PPKPS 2407

RESULT 12
017610
ID      017610      PRELIMINARY;      PRT;      474 AA.
AC      017610;
DT      01-JAN-1998 (TREMBlrel. 05, Created)
DT      01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT      01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE      C28D4.2 PROTEIN.
GN      C28D4.2
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
OX      NCBI_TaxID=6239;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      McMurray A.;
RL      Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR      EMBL; 282259; CAB05129.1; -.
DR      InterPro: IPR002573; Choline_kinase.
DR      Pfam: PF01633; Choline_kinase; 1.
SQ      SEQUENCE 474 AA; 54628 MW; DDF1LC97A1542FFC CRC64;

Query Match      7.2%; Score 89.5; DB 5; Length 474;
Best Local Similarity 24.1%; Pred. No. 2.2;
Matches 59; Conservative 29; Mismatches 82; Indels 75; Gaps 15;

QY      27 TQDC-----SFQHS-PISSDFAVKIREL-SDYLLQDPVTVVASNLQDEELCGGLWRL 76
Db      65 TTDCVDLKKVKFSKFDSSAPISGEILFRFLCAKYL-----GGAWRK 106
QY      77 VLAQRMERLKVASKKMOGLERVENTEIHFTKCAFOPPPSCLR-FVOTNISRLQET- 134
Db      107 VKIEEF--RIRAITGG-MSNLLFLVELPAH-LTPIQMEPEKALLRVHCQSDIQLLSESV 162
QY      135 -----SQVLAKPWITRQNSRCLELQC-----OPDSSTLPPPWSPR--PLEATA 178
Db      163 VFTLLSERNLGPKMLGVPPGGRFQFIPSRALQCLEISKPLGSLKIAPIVARVHTLDAP 222
QY      179 FPAPQPLLPLLLVGLLLAAACLHWQTRRRTTP---RPGE-----QVPPVPSPQD 229
Db      223 KPEPQ-----TLQTARQWLERF---KKTAGERPIEMYLQAKVPKSDYFST 266
QY      230 LLIVE 234
Db      267 ITVAQ 271

RESULT 13
090WT1
ID      090WT1      PRELIMINARY;      PRT;      270 AA.
AC      090WT1;
DT      01-MAY-2000 (TREMBlrel. 13, Created)
DT      01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT      01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE      NKP44RG2 PROTEIN.
GN      NKP44RG2.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      TISSUE-LYMPHOID;
RA      Cantoni C., Biassoni R.;
RT      "NKP44 related genes.";
RL      Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC      CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC      DOMAIN.
DB      EMBL; AJ010100; CAB52290.1; -.

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DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00409; Ig; 1.
SQ SEQUENCE 270 AA; 29678 MW; 327AD57A5634AE46 CRC64;

Query Match 7.1%; Score 88.5; DB 4; Length 270;
Best Local Similarity 23.0%; Pred. No. 1.5;
Matches 63; Conservative 22; Mismatches 112; Indels 77; Gaps 15;

QY 7 AWSPTTIVLLILLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQD 66
Db 2 AWRALHPLLLLLLPFGSQAKQVLSVAGOTLTVRQ-----YPT----- 45
QY 67 EELCGGLW-----RLVLAQR-----WNERLKTAVGSKMQGLLRVNTETI- 105
Db 46 ----GSLYEKKGWCKEASALVCIRLVTSRPRTMANTSRF-TIWDPDGAEFTVTMDLR 100
QY 106 -----HFVTKCAFOPPPSCLEFVOTNISRLLOETSEOLVALKPWITRONFSRCLELQ-CQ 159
Db 101 EEDSGHY--WCRIYRPSD--NSVSKSVRFYLVSPASASTOTPTPRDLVSSQTQTQSCV 156
QY 160 PDS-----STLPPHSP-RPLEATAPQ-----PPLLLLLLPV--GLL--- 197
Db 157 PPTAGARQAPESPSTIVPSPSPPLVPLFSRPNQNTLRPGPAAPALVPVFCGLLVAK 216
QY 198 -LLAAACWCLHWQRTTRTPRGEQV--PPVPSQP 228
Db 217 SLVLSALLVWVLRNHRHQGRSLHPAQR PQ 250

RESULT 14

Q9AWJ4 Q9AWJ4 PRELIMINARY; PRT; 404 AA.
AC Q9AWJ4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE P0489A05.3 PROTEIN.
GN P0489A05.3.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0489A05."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003105; BAB32983.1;
SQ SEQUENCE 404 AA; 43109 MW; 7CA66FDE7772A64B CRC64;

Query Match 7.1%; Score 88.5; DB 10; Length 404;
Best Local Similarity 26.1%; Pred. No. 2.3;
Matches 66; Conservative 24; Mismatches 88; Indels 75; Gaps 17;

QY 33 QHSPISDF--AVKIRELSYLLQDYPVTVASNL-----QDEELCGGLRLVL 78
Db 107 RHFSLFSFLEKVIQITPLKYVSNVNYPLKPNQTFITLNYQKNSEPOLCKRFW---- 162
QY 79 AQRWMLKTVAGSKMGQ----LLRVNT--EIHFTKCAFOPPPSCLEFVOTNI---SRL 130
Db 163 -STWQSNAGY-GSRAGGSERLRRSPMLVPPPPPPRASAAGVPNIALTSRA 220
QY 131 LOETSEOLVALKPWITRONFSR----CLELQ--CQDSSITLP-----PPWSPRPLEAT 177
Db 221 LSATG-----TPTTSSSILRPLHCLLPPLRARPSPSLPLPLPQAPPHPLP---P 271

QY 178 APTAPQPPPLLLLLL-----PV---GLL-----LLAAACWCLHWQRTTRRTPR 216
Db 272 PPTARAPPPIAVLCLLRCPLYLKPKPPVAGGLFVAHSALTAVLCAGCV--RLHRRPLR 329
QY 217 P-GEQVPPVPSP 227
Db 330 PPSSELLPLSRAP 342

RESULT 15

O75064 O75064 PRELIMINARY; PRT; 1386 AA.
AC O75064;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE KIAA0476 PROTEIN.
GN KIAA0476.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=98116662; PubMed=9455484;
RA Seki N., Ohira M., Nagase T., Ishikawa K., Miyajima N., Nakajima D.,
RA Nomura N., Ohara O.;
RT "Characterization of cDNA clones in size-fractionated cDNA libraries
RL DNA Res. 4:345-349(1997).
DR EMBL; AB007945; BAA32321.1;
DR InterPro: IPR001194; DENN.
DR InterPro: IPR002885; PPR.
DR Pfam: PF01535; PPR; 1.
DR Pfam: PF02141; DENN; 1.
SQ SEQUENCE 1386 AA; 152296 MW; BE960E7169A7EFDA CRC64;

Query Match 7.1%; Score 88.5; DB 4; Length 1386;
Best Local Similarity 23.1%; Pred. No. 8.6;
Matches 53; Conservative 28; Mismatches 85; Indels 63; Gaps 12;

QY 21 SSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELC---GGLWRL 76
Db 1104 SAGASGSKDAPVPGP-----GPVLSRRICLA--LDEPQLCNHMGASRR 1148
QY 77 VLAQRWMLKTVAGSKMGGLLRVNTETIHFVTKCAFOPPPSCLEFVOTNISRLLOETSE 136
Db 1149 VESGAWAYLSPLVLRKELESIVENEGSEV-----LALPELPSAHPFIIFWLLWYFQRL-- 1201
QY 137 QLVALKPWITRONFSRCLELOCO-PDSSTLPPPW-SPRPLEA-----TAPTAPQPP 185
Db 1202 RLPSTLPGVLVAS-----CDGPSHQAPSPMLTPDPAVSQVRLMDVLPDPNSCPP 1253
QY 186 LLLLLLPPVGLLLAAACWCLHWQRTTRTPRGEQVPPVPSQDILLVE 234
Db 1254 LYVL-----WRVHSQ-IPQRVWPG-----PVPASLSLALLE 1284

Search completed: April 1, 2002, 06:25:43
Job time: 619 sec

Mon Apr 1 06:15:20 2002

us-08-162-407-6.rspt

Page 7

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 1, 2002, 06:13:54 ; Search time 77.69 Seconds
(without alignments)
224.060 Million cell updates/sec

Title: US-08-162-407-6
Perfect score: 1242
Sequence: 1 MVLAPAWSTYLLLLLLL.....RPGQVPPVSPQDLLLVEH 235

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	235	16 AAR67541	Human flt-3 ligand
2	1242	100.0	235	20 AAW67769	Human flt-3 ligand
3	1242	100.0	235	21 AAY69719	Full length wild t
4	1242	100.0	235	22 AAB20192	Human flt-3 ligand
5	1236	99.5	235	16 AAR66175	Human S86/S109 Flt
6	1236	99.5	235	22 AAB20194	Human flt-3 ligand
7	1124	90.5	212	21 AAY69721	Human flt-3 ligand
8	1114	89.7	209	19 AAW69007	Human flt-3 recept
9	1114	89.7	209	21 AAY69720	Mature wild type h
10	1110	89.4	209	21 AAY69723	Human flt-3 mutein
11	1110	89.4	209	21 AAY69726	Human flt-3 mutein

12	1110	89.4	209	21	AAY69727	Human flt-3 mutein
13	1110	89.4	209	21	AAY69729	Human flt-3 mutein
14	1108	89.2	209	21	AAY69722	Human flt-3 mutein
15	1108	89.2	209	21	AAY69724	Human flt-3 mutein
16	1107	89.1	209	21	AAY69728	Human flt-3 mutein
17	1100	88.6	209	21	AAY69725	Human flt-3 mutein
18	970	78.1	185	22	AAB20195	Human flt-3 ligand
19	895.5	72.1	294	21	AAY58204	Canine flt-3 ligand
20	894.5	72.0	291	21	AAY58210	Canine flt-3 ligand
21	894	67.1	178	22	AAB20193	Human flt-3 ligand
22	797.5	64.2	268	21	AAY58206	Canine mature Flt-
23	796.5	64.1	276	21	AAY58207	Canine flt-3 ligand
24	791.5	63.7	265	21	AAY58211	Feline mature Flt-
25	768.5	61.9	231	16	AAR67540	Mouse flt-3 ligand
26	768.5	61.9	231	20	AAW67768	Murine flt-3 ligand
27	768.5	61.9	231	22	AAB20186	Mouse flt-3 ligand
28	768	61.8	232	16	AAR66177	Mouse flt-3 ligand
29	764	61.5	232	22	AAB20189	Mouse flt-3 ligand
30	745	60.0	150	19	AAW77930	Flt3 ligand FLT10C
31	745	60.0	150	19	AAW69054	Human flt-3 recept
32	740.5	59.6	377	19	AAW78124	Chimeric receptor
33	739	59.5	143	19	AAW77926	Flt3 ligand FLT3C
34	739	59.5	143	19	AAW69050	Human flt-3 recept
35	737.5	59.4	349	19	AAW83289	Human flt-3 ligand
36	737.5	59.4	349	19	AAW78005	Flt3L 1-139/IgG2b/
37	736.5	59.3	340	19	AAW83291	Human flt-3 ligand
38	736.5	59.3	349	19	AAW83286	Human flt-3 ligand
39	736.5	59.3	523	19	AAW78008	Trimeric Flt3L-G-C
40	735	59.2	140	19	AAW77911	Human flt-3 ligand
41	735	59.2	140	19	AAW69035	Human flt-3 recept
42	735	59.2	144	19	AAW77928	Flt3 ligand FLT4C
43	735	59.2	144	19	AAW69052	Human flt-3 recept
44	735	59.2	313	19	AAW83294	Human flt-3 ligand
45	733.5	59.1	286	19	AAW83303	Human flt-3 ligand

ALIGNMENTS

RESULT 1
AAR67541
ID AAR67541 standard; Protein; 235 AA.
AC AAR67541;
XX
XX 05-AUG-1995 (first entry)
XX Human flt-3 ligand.
XX
XX Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..26
XX /label- Sig_peptide
XX /note- "signal peptide may extend to position 27"
XX Domain 27..182
XX /label- "Extracellular domain
XX /label- "Extracellular domain may start at
XX position 28"
XX Domain 183..205
XX /label- Transmembrane_domain
XX Domain 206..235
XX /label- Cytoplasmic_domain
XX
XX EP627487-A.
XX
XX 07-DEC-1994.
XX
XX 19-MAY-1994; 94EP-0303575.
XX
XX 24-MAY-1993; 93US-0068394.

PR 12-AUG-1993; 93US-0106463.
 PR 25-AUG-1993; 93US-0111758.
 PR 03-DEC-1993; 93US-0162407.
 PR 07-MAR-1994; 94US-0209502.
 PR 11-MAY-1994; 94US-0243545.
 XX (IMV) IMMUNEX CORP.
 PA Beckmann MP, Lyman SD;
 XX WPI: 1995-008071/02.
 DR N-PSDB; AAQ79079.
 XX Isolated ligands for flt 3 receptors - useful for treating
 PT anaemia, AIDS and various cancers
 PS Disclosure; Page 29-30; 33pp; English.
 XX A human T-cell lambda-gt10 random primed cDNA library was
 CC screened with a fragment corresponding to the extracellular
 CC domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AAQ79076)
 CC to isolate human flt3-L cDNA. Flt-3 stimulates progenitor and
 CC stem cells, and can be used e.g. in gene therapy protocols.
 XX Sequence 235 AA;
 SQ

Query Match 100.0%; Score 1242; DB 16; Length 235;
 Best Local Similarity 100.0%; Pred. No. 3.6e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLAPAWSPPTVLLLLSSGLSGTQCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
 Db 1 mtvlapawspptvlllllssglsqtcfsqhspsissdfavkirelsydlldypvtv 60
 QY 61 ASNLDEELCGGLWRLVLAQRWMLKTVAGSKMQLLRYVTEIHFTVKCAFQPPPSCL 120
 Db 61 asnldeelcggglwrlvlagrwmrlktvagskmgllervnteihfvtkcafqpplscl 120
 QY 121 RFVQTNISRLQETSQQLVAKPWITRQNFSCLELQCPDSTLPPWSPRPLEATAPT 180
 Db 121 rfvtqtnisrlqetseqqlvalkpwtirqnfscrlclqcpdstlppwsprrpleatapt 180
 QY 181 APQPPLLLLLPVGLLLAAWCLHWQTRRRTPRGSGVPPVPSQDLLLLVEH 235
 Db 181 apqpplllllpvglllalaawclhwqtrrrtrtprgsgvppvpqgdllllveh 235

RESULT 2
 ID AAW67769 standard; Protein; 235 AA.
 XX AAW67769;
 AC
 XX 25-MAR-1999 (first entry)
 DT
 XX Human flt3-ligand.
 DE
 XX Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L;
 KW immunogenic; autoimmune disease; organ transplantation; food allergy;
 KW tissue transplantation.
 OS Homo sapiens.
 XX WO9857655-A1.
 PN
 XX 23-DEC-1998.
 PD
 XX 12-JUN-1998; 98WO-US12085.
 PF
 XX 17-JUN-1997; 97US-0877421.
 PR
 XX (IMV) IMMUNEX CORP.
 PA

XX Abbott NM, Mowat AM, Viney JL;
 PI WPI: 1999-070422/06.
 DR N-PSDB; AAV81506.
 DR
 XX Methods for initiating or enhancing antigen specific immune
 PT tolerance - by using murine or human flt3 ligand
 PS Claim 1; Page 14-15; 25pp; English.
 XX A method has been developed of initiating or enhancing: (i) an antigen-
 CC specific immune tolerance; or (ii) immunotolerance of a therapeutic
 CC immunogenic molecule by addition of a polypeptide, before, after or with
 CC the mucosal administration of an immunotolerising amount of the antigen
 CC or therapeutic molecule, respectively. The polypeptide is capable of
 CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3
 CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino
 CC acids 28-y of human flt3-L, where y is an amino acid between 160-235;
 CC and c) a polypeptide that has at least 90% identity to the polypeptides
 CC of either (a) or (b). The method ameliorates the effects of autoimmune
 CC diseases, food allergies or organ or tissue rejection following
 CC transplantation. Administration of flt3-L allows lower doses of antigens
 CC to be used in vivo for mucosally administered antigens. The present
 CC sequence represents human flt3-L.
 XX Sequence 235 AA;
 SQ

Query Match 100.0%; Score 1242; DB 20; Length 235;
 Best Local Similarity 100.0%; Pred. No. 3.6e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLAPAWSPPTVLLLLSSGLSGTQCSFQHSPISSDFAVKIRELSYLLQDYPVTV 60
 Db 1 mtvlapawspptvlllllssglsqtcfsqhspsissdfavkirelsydlldypvtv 60
 QY 61 ASNLDEELCGGLWRLVLAQRWMLKTVAGSKMQLLRYVTEIHFTVKCAFQPPPSCL 120
 Db 61 asnldeelcggglwrlvlagrwmrlktvagskmgllervnteihfvtkcafqpplscl 120
 * QY 121 RFVQTNISRLQETSQQLVAKPWITRQNFSCLELQCPDSTLPPWSPRPLEATAPT 180
 Db 121 rfvtqtnisrlqetseqqlvalkpwtirqnfscrlclqcpdstlppwsprrpleatapt 180
 QY 181 APQPPLLLLLPVGLLLAAWCLHWQTRRRTPRGSGVPPVPSQDLLLLVEH 235
 Db 181 apqpplllllpvglllalaawclhwqtrrrtrtprgsgvppvpqgdllllveh 235

RESULT 3
 ID AAY69719 standard; Protein; 235 AA.
 XX AAY69719;
 AC
 XX 05-JUL-2000 (first entry)
 DT
 XX Full length wild type human flt-3 protein.
 DE
 XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia.
 XX Homo sapiens.
 OS
 XX WO200001823-A2.
 PN
 XX 13-JAN-2000.
 PD

XX 25-JUN-1999; 99WO-US14296.
 XX 02-JUL-1998; 98US-0109100.
 XX (IMMV) IMMUNEX CORP.
 XX Graddis TJ, McGrew JT;
 XX WPI; 2000-182115/16.
 XX N-PSDB; AAZ59064.
 XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 XX immune response stimulation or treatment of pathological conditions
 XX contains amino acid substitutions at positions 8, 84, 118 or 122 .
 XX
 PS Claim 1; Page 72-73; 90pp; English.
 CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (this sequence) or mature (AAV69720) flt3-L
 CC polypeptides. The flt3-L protein binds cell surface tyrosine kinase
 CC receptors and regulate growth and differentiation of hematopoietic
 CC progenitor cells. The flt3-L protein can be used to induce cellular
 CC expansion (especially in vivo) or differentiation, e.g. in
 CC hematopoietic, natural killer (NK) or dendritic cells, especially in the
 CC presence of growth factors such as interleukins, colony stimulating
 CC factors or protein kinases. The protein can also modulate, augment or
 CC enhance a patient's immune response and can be used to treat an immune
 CC disorder (e.g. allergy, autoimmunity or immunosuppression). The protein
 CC may be used to treat a pathological condition e.g. myelodysplasia,
 CC aplastic anemia, HIV infection, breast, small cell lung, testicular or
 CC ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
 CC leukemia.
 XX
 SQ Sequence 235 AA;

Query Match 100.0%; Score 1242; DB 21; Length 235;
 Best Local Similarity 100.0%; Pred. No. 3.6e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVLAPAWSPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDPYPTV 60
 Db 1 mtvlapawspttylllllssglsqtdcsfghpsissdfavkirelsydlldqypvtv 60
 QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMGLLERNVTEHFYTKCAFQPPPSCL 120
 Db 61 asnlqdeecgglwrlvlagrwmrlktvagskmgllervntelhfvtkcafqpptscl 120
 QY 121 RFVOTNISRLLETSQVQLVKPWITRQNFSCLELQCPDSSITLPPWSPRPLEATAPT 180
 Db 121 rfvgtnisrllqetseqlvklpwitrgnfsclclqcpdsstlppwspripateapt 180
 QY 181 APQPPILLLLLPVGLLLAAWCLHWQRTTRRRPRGEGVPPSPQDLLLVEH 235
 Db 181 apqpplllllpvglllaawclhwgrtrrrprgqevppspqdlllveh 235

RESULT 4
 AAB20192
 ID AAB20192 standard; Protein; 235 AA.

XX AAB20192;
 AC AAB20192;
 XX 14-MAY-2001 (first entry)
 DT Human Flt-3 ligand.
 XX Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
 KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;
 KW lymphoma; autoimmune disease; infection; gene therapy.

OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..26
 FT /label= Signal_peptide
 FT Protein 27..235
 FT /label= Mature_protein
 FT Domain 27..182
 FT /label= Extracellular_domain
 FT Domain 183..205
 FT /label= Transmembrane_domain
 FT Domain 206..235
 FT /label= Cytoplasmic_domain
 XX
 XX WO200109303-A2.
 XX 08-FEB-2001.
 XX 31-JUL-2000; 2000WO-US20679.
 XX 30-JUL-1999; 99US-0146170.
 XX (VICA-) VICAL INC.
 XX Hermanson GG;
 XX WPI; 2001-123319/13.
 XX N-PSDB; AAF30310.
 XX Immunogenic compositions comprising Flt-3 ligand encoding
 XX polynucleotide and one or more antigen, or cytokine encoding
 XX polynucleotides, useful for suppressing tumour growth and for treating
 XX autoimmune diseases. (e.g. rheumatoid arthritis) .
 XX
 PS Claim 2; Page 132-133; 149pp; English.
 CC The present sequence is that of human Fms-like tyrosine kinase
 CC (Flt-3 ligand). The invention is directed to enhancing the
 CC immune response of a vertebrate to an antigen or a cytokine by
 CC administering in vivo, into a tissue of a vertebrate, a Flt-3
 CC ligand-encoding polynucleotide, and 1 or more antigen- or
 CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
 CC polynucleotide may encode the present full-length human Flt-3
 CC ligand polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185,
 CC or 27-235 of the ligand. The polynucleotides are incorporated
 CC into the cells of the vertebrate in vivo, and a prophylactically
 CC or therapeutically effective amount of Flt-3 ligand and 1 or more
 CC antigens or cytokines is produced in vivo. Pharmaceutical
 CC compositions comprising the polynucleotides are useful for
 CC suppressing tumour growth in a mammal. The tumour is melanoma,
 CC glioma or lymphoma, particularly B-cell lymphoma. They can also
 CC be used for the prophylactic and/or therapeutic treatment of:
 CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
 CC and C in humans), parasitic (e.g. malaria) and fungal infections;
 CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
 CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
 CC Various other examples of these diseases are given in the
 CC specification.
 XX
 SQ Sequence 235 AA;

Query Match 100.0%; Score 1242; DB 22; Length 235;
 Best Local Similarity 100.0%; Pred. No. 3.6e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDPYPTV 60
 Db 1 mtvlapawspttylllllssglsqtdcsfghpsissdfavkirelsydlldqypvtv 60
 QY 61 ASNLQDEELCGGLWRLVLAQRWMLKTVAGSKMGLLERNVTEHFYTKCAFQPPPSCL 120
 Db 61 asnlqdeecgglwrlvlagrwmrlktvagskmgllervntelhfvtkcafqpptscl 120

QY 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLELOCPDSTLPPWSPRPLEATAPT 180
|||||
Db 121 rfvtuinsrlilqetseqvalkpwtitronfsrclclqcpdsstlppwsprrleatapt 180
|||||
QY 181 AQOPPLLLLLLVGLLLAAAWCLHWQTRRRTPRGEQVPPVPSQDLLLVEH 235
|||||
Db 181 apqpplllllllpvgllllaaawclhwqtrrrtrprgeqvpvpsqdllllveh 235
|||||
RESULT 5
AAR66175
ID AAR66175 standard; Peptide; 235 AA.
XX
AC AAR66175;
XX
DT 10-AUG-1995 (first entry)
XX
DE Human S86/S109 Flt3 ligand peptide sequence.
XX
KW Flt3 ligand; tyrosine kinase receptor ligand.
XX
OS Homo sapiens.
XX
PN WO9426891-A.
XX
PD 24-NOV-1994.
XX
PF 18-MAY-1994; 94WO-US05150.
XX
PR 19-MAY-1993; 93US-0065231.
PR 07-JUL-1993; 93US-0089263.
PR 16-JUL-1993; 93US-0092549.
PR 13-AUG-1993; 93US-0106340.
PR 24-AUG-1993; 93US-0112391.
PR 19-NOV-1993; 93US-0155111.
PR 03-DEC-1993; 93US-0162413.
XX
PA (INRM) INST NAT SANTE & RECH.MEDICALE.
PA (SCHE) SCHERING CORP.
XX
PI Birnbaum D, Culpepper JA, Hannum CH, Lee FD;
XX
XX WPI; 1995-006787/01.
DR N-PSDB; NAO79642.
XX
XX New ligand for the Flt3 tyrosine kinase receptor - and related
PT nucleic acid, vectors, host cells and antibodies, useful for
PT treating abnormal cell physiology and proliferation, e.g. cancer,
PT also for diagnosis and drug screening
XX
PS Claim 11; Page 76-77; 90pp; English.
XX
XX A cDNA library from the human stromal cell line 29SV48, in
CC pME18S, was screened with an 800 bp fragment derived from
CC mouse clone T118. This fragment encompasses the coding region
CC conserved between two mouse clones, T118 and T110. Approx. 20
CC positive clones were selected and partially sequenced. Two
CC clones, S86 and S109, were found to be approx. 75% homologous
CC to the mouse clones over the first 163 AAs. Clone S86 continued
CC to show homology to T110 until the stop codon, although to a
CC lesser degree, for an overall homology of 68%. Clones T118 and
CC S109 do not show homology to each other or to the other clones
CC after mouse residue 163 (human residue 160). An additional mouse
CC clone designated MB8 has a 29 AA insert at the junction between
CC the common and divergent portions of the mouse ligand.
XX
SQ Sequence 235 AA;

Query Match 99.5%; Score 1236; DB 16; Length 235;
Best Local Similarity 99.6%; Pred. No. 1.3e-108;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTLAPAWSPPTTYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVTY 60
|||||
Db 1 mtlapawsppttylllllssglsgtqdcsfqhsplssdfavkirelsyldqypvtv 60
|||||
QY 61 ASNLQDEELCCGLWRLVLAQRWMERLKTAVGSKMGQLLERVNTTEHFVTKCAFQPPSPCL 120
|||||
Db 61 asnlqdeelcglwrlvlagrwmrklktavagskmqgllervntelhfvtkcafqpsspcl 120
|||||
QY 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLELOCPDSTLPPWSPRPLEATAPT 180
|||||
Db 121 rfvtuinsrlilqetseqvalkpwtitronfsrclclqcpdsstlppwsprrleatapt 180
|||||
QY 181 AQOPPLLLLLLVGLLLAAAWCLHWQTRRRTPRGEQVPPVPSQDLLLVEH 235
|||||
Db 181 apqpplllllllpvgllllaaawclhwqtrrrtrprgeqvpvpsqdllllveh 235
|||||
RESULT 6
AAB20194
ID AAB20194 standard; Protein; 235 AA.
XX
AC AAB20194;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human Flt-3 ligand.
XX
KW Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;
XX lymphoma; autoimmune disease; infection; gene therapy.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Peptide 1..26
FT Protein /label= Signal_peptide
FT FT 27..235
FT FT /label= Mature_protein
FT FT 27..182
FT FT /label= Extracellular_domain
FT FT 183..205
FT FT /label= Transmembrane_domain
FT FT 206..235
FT FT /label= Cytoplasmic_domain
XX
XX WO200109303-A2.
XX
XX 08-FEB-2001.
XX
XX 31-JUL-2000; 2000WO-US20679.
XX
XX 30-JUL-1999; 99US-0146170.
XX
XX (VICA-) VICAL INC.
XX
XX Hermanson GG;
XX
XX WPI; 2001-123319/13.
XX N-PSDB; AAF30312.
XX
XX Immunogenic compositions comprising Flt-3 ligand encoding
PT polynucleotide and one or more antigen, or cytokine encoding
PT polynucleotides, useful for suppressing tumour growth and for treating
PT autoimmune diseases (e.g. rheumatoid arthritis)
XX
PS Claim 2; Page 137-138; 149pp; English.
XX
XX The present sequence is that of human Fms-like tyrosine kinase
CC (Flt-3 ligand). The invention is directed to enhancing the
CC immune response of a vertebrate to an antigen or a cytokine by
CC administering in vivo, into a tissue of a vertebrate, a Flt-3
CC ligand-encoding polynucleotide, and 1 or more antigen- or

cytokine-encoding polynucleotides. The Flt-3 ligand-encoding polynucleotide may encode the present full-length human Flt-3 ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235 of the Flt-3 ligand. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Flt-3 ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of: (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections; (b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs. Various other examples of these diseases are given in the specification.

XX Sequence 235 AA;

Query Match 99.5%; Score 1236; DB 22; Length 235;
 Best Local Similarity 99.6%; Pred. No. 1.3e-108;
 Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLPAWSPTTYLLLLLLSSGLSGTQCSFQHSPISSDFAVKIRELSDYLLQDPYPTV 60
 Db 1 mtvlpawspttyllllllssglsgtqcsfghspissdfavkirelsdyllqdpv 60

QY 61 ASNLQDEELCGRLVLAQRWRELKTVAGSKMGLLERNVTEHFVTKCAFQPPSCL 120
 Db 61 asnlqdeecogalwrlvlagrwerlktvagskmqgllervnteihfvtkcafppsc 120

QY 121 RFVQTNISRLLOETSEOLVALKPWITRONFSKCLELQCPDSSSTLPWSPRPLEATAPT 180
 Db 121 rfvtgnisrllqetseqlvalkpwttrnfscrlclqcpdssstlppwsprip 180

QY 181 APQPPLLLLLVGLLLAAAWCLHWQTRRRTRPRGQVPPVPSQDILLVEH 235
 Db 181 apqppllllllpvgllllaaawclhwqtrrrtrprgeqvppvpsqdillveh 235

RESULT 7
 AAY69721
 ID AAY69721 standard; Protein; 212 AA.
 AC AAY69721;
 XX
 XX
 XX 05-JUL-2000 (first entry)
 XX
 DE Human flt-3 mutein L-3H.
 XX
 KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autolymnity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001823-A2.
 XX
 PD 13-JAN-2000.
 XX
 XX 25-JUN-1999; 99WO-US14296.
 PF
 XX
 PR 02-JUL-1998; 98US-0109100.
 XX
 PA (IMV) IMMUNEX CORP.
 XX

PI Graddis TJ, McGrew JT;
 XX
 DR WPI; 2000-182115/16.
 XX
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion.
 PT Immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122
 XX
 PS Claim 4; Page 79-80; 90pp; English.
 XX
 CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAY69713) or mature (AAY69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt-3
 CC ligands and comprises the L-3H mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
 CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.
 XX
 SQ Sequence 212 AA;

Query Match 90.5%; Score 1124; DB 21; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4.2e-98;
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 SCTQDCSFQHSPISSDFAVKIRELSDYLLQDPYPTVNASLQDEELCGRLVLAQRWME 84
 Db 2 sctqdcfsqhspsissdfavkirelsdyllqdpvptvasnlqdeecgllvlagrme 61

QY 85 RLKTVAGSKMGLLERNVTEHFVTKCAFQPPSPSCIRFVQTNISRLLOETSEOLVALKPW 144
 Db 62 rlktvagskmqgllervnteihfvtkcafpppsclrfvtgnisrllqetseqlvalkp 121

QY 145 ITRQNFSCLELQCPDSSSTLPWSPRPLEATAPTAPQPPLLLLLVGLLLAAAWC 204
 Db 122 itrqnfsrclclqcpdssstlppwspripseaptapqpplllllpvgllllaaawc 181

QY 205 LHWQTRRRTRPRGQVPPVPSQDILLVEH 235
 Db 182 lhwqtrrrtrprgeqvppvpsqdillveh 212

RESULT 8
 AAY69007
 ID AAY69007 standard; peptide; 209 AA.
 XX
 AC AAY69007;
 XX
 XX 01-OCT-1998 (first entry)
 XX
 XX Human flt-3 receptor agonist.
 DE
 DE
 XX
 KW Human; flt-3 receptor agonist; hematopoietic cell stimulation; cancer;
 KW bone marrow reconstitution; hematological disease; immune deficiency;
 KW drug-induced myelosuppression; renal dialysis; gene therapy; infection;
 KW congenital metabolic disease; neurological disease; therapy;
 KW dendritic cell production.
 XX
 OS Homo sapiens.
 XX
 PN WO9818923-A1.
 XX
 XX 07-MAY-1998.
 PD

XX 23-OCT-1997; 97WO-US18700.
 XX
 PR 25-OCT-1996; 96US-0030094.
 XX
 PA (SEAR) SEARLE & CO G D.
 XX
 PI Feng Y, McKearn JP, McWherter CA, Minnerly JC, Minster NI;
 PI Staten NR, Streeter PR, Woulfe SL;
 XX WPI; 1998-272218/24.
 XX
 DR Rearranged flt-3 receptor agonists and nucleic acids encoding them -
 PT used to stimulate production of haematopoietic and dendritic cells,
 PT for treatment of haematological diseases, bone marrow reconstitution
 PT and in gene therapy
 XX
 PS Disclosure; Page 9-10; 158pp; English.
 XX
 CC This sequence represents a rearranged human flt-3 receptor agonists of
 CC the invention. The agonists have a modified flt-3 ligand amino acid
 CC sequence. The agonists are used to stimulate production of haematopoietic
 CC cells in vivo (e.g. in a subject about to donate blood) or for ex vivo
 CC expansion for subsequent transplantation, e.g. to reconstitute bone
 CC marrow after chemotherapy, disease etc., or to treat haematological
 CC disease such as drug-induced myelosuppression, defects caused by
 CC infections, burns or renal dialysis. Optionally ex vivo expanded cells
 CC are transduced with a gene therapy vector for treating e.g. congenital
 CC metabolic diseases, immune deficiency, neurological disease, cancer and
 CC infections. The agonists can also be used in the treatment of tumours,
 CC infections and autoimmune disease, when administered optionally with an
 CC antigen. The agonist can also be used in the production of dendritic
 CC cells for use as an immunising adjuvant for treatment disorders including
 CC acquired immune deficiency syndrome. Compared with native ligands, the
 CC new agonists have better stimulatory activity, reduced side effects
 CC and/or better physical properties such as solubility, stability or refold
 CC efficiency. When used together with other stimulatory agents, the
 CC agonists provide a synergistic effect.
 XX
 SQ Sequence 209 AA;

Query Match 89.7%; Score 1114; DB 19; Length 209;
 Best Local Similarity 100.0%; Pred. No. 3.6e-97;
 Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TDQCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLDQDEELCGGLRLVLAQRWMLR 86
 DB 1 tqdcsfqhspsissdfavkirelsylylqdyptvtvasnlqdeecgglrwlvlqgrwmerl 60

QY 87 KTVAGSKMQLLRLVNTFHTKCAFPQPPSCIRFVQTNISRLLOETSEQLVAKPWIT 146
 DB 61 ktvagskmqgllervntelhfvtkcacfpppsclrfvqtnisrllqetseqvlakpwit 120

QY 147 RQNFSCRLELCQPDSTLPPWSPRPLEATAPQPPILLLLLPVGLLLAAWCLH 206
 DB 121 rqnfsrclclqcpdssatlpwpsrpplseataptapqpilllllpvglllaaawclh 180

QY 207 WQTRRRTPRPGEQVPVPSQDILLVEH 235
 DB 181 wqtrrrtrprpggeqvppvpsqdillveh 209

RESULT 9
 ID AAY69720
 XX AAY69720 standard; Protein; 209 AA.
 AC
 XX
 XX 05-JUL-2000 (first entry)
 XX
 DE Mature wild type human flt-3 protein.
 XX

KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autolmmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia.
 XX Homo sapiens.
 XX OS
 XX PN WO200001823-A2.
 XX PD 13-JAN-2000.
 XX PF 25-JUN-1999; 99WO-US14296.
 XX PR 02-JUL-1998; 98US-0109100.
 XX PA (IMMV) IMMUNEX CORP.
 XX Graddis TJ, McGrew JT;
 XX WPI; 2000-182115/16.
 XX N-PSDB; AAZ59064.
 CC Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 CC immune response stimulation or treatment of pathological conditions
 CC contains amino acid substitutions at positions 8, 84, 118 or 122 .
 PS Claim 1; Page 89-90; 90pp; English.
 XX
 CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAV69719) or mature (this sequence) flt3-L
 CC polypeptides. The flt3-L protein binds cell surface tyrosine kinase
 CC receptors and regulate growth and differentiation of hematopoietic
 CC progenitor cells. The flt3-L protein can be used to induce cellular
 CC expansion (especially in vivo) or differentiation, e.g. in
 CC hematopoietic, natural killer (NK) or dendritic cells, especially in the
 CC presence of growth factors such as interleukins, colony stimulating
 CC factors or protein kinases. The protein can also modulate, augment or
 CC enhance a patient's immune response and can be used to treat an immune
 CC disorder (e.g. allergy, autoimmunity or immunosuppression). The protein
 CC may be used to treat a pathological condition e.g. myelodysplasia,
 CC aplastic anemia, HIV infection, breast, small cell lung, testicular or
 CC ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
 CC leukemia.
 XX
 SQ Sequence 209 AA;

Query Match 89.7%; Score 1114; DB 21; Length 209;
 Best Local Similarity 100.0%; Pred. No. 3.6e-97;
 Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TDQCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLDQDEELCGGLRLVLAQRWMLR 86
 DB 1 tqdcsfqhspsissdfavkirelsylylqdyptvtvasnlqdeecgglrwlvlqgrwmerl 60

QY 87 KTVAGSKMQLLRLVNTFHTKCAFPQPPSCIRFVQTNISRLLOETSEQLVAKPWIT 146
 DB 61 ktvagskmqgllervntelhfvtkcacfpppsclrfvqtnisrllqetseqvlakpwit 120

QY 147 RQNFSCRLELCQPDSTLPPWSPRPLEATAPQPPILLLLLPVGLLLAAWCLH 206
 DB 121 rqnfsrclclqcpdssatlpwpsrpplseataptapqpilllllpvglllaaawclh 180

QY 207 WQTRRRTPRPGEQVPVPSQDILLVEH 235
 DB 181 wqtrrrtrprpggeqvppvpsqdillveh 209

RESULT 10

AAY69723
 ID AAY69723 standard; Protein; 209 AA.
 AC AAY69723;
 DT 05-JUL-2000 (first entry)
 DE Human flt-3 mutein K84E.
 DE
 KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001823-A2.
 XX
 PD 13-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US14296.
 XX
 PR 02-JUL-1998; 98US-0109100.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Graddis TJ, McGrew JT;
 XX
 DR WPI; 2000-182115/16.
 XX
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122
 XX
 PS Claim 4; Page 84-85; 90pp; English.
 XX
 CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt-3
 CC ligands and comprises the K84E mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
 CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.
 XX
 SQ Sequence 209 AA;
 Query Match 89.4%; Score 1110; DB 21; Length 209;
 Best Local Similarity 99.5%; Pred. No. 8.5e-97;
 Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 27 TQCSFQHSPISSFAVKIRELSYLLQDYPTVTVASNLQDEELGGLWRLVLAQRWMERL 86
 Db 1 tqdcsfghspissdfavkirelsdyllqdyptvtvasnlqdeecgglwrlvlaqrwmerl 60
 QY 87 KTVAGSKMGLLRRVNTIEHFVKCAFPQPPSCULRFVOTNISRLLQETSEQLVAKPWIT 146
 Db 61 ktvagskmglrrvntiehfvtcatqpppsclrfvqtnisrllqetseqlvakpwit 120

QY 147 RQNFRCLELCQCPDSSLTLPWPSPRPLEATAPQPPILLILLPVGILLAAACWLH 206
 Db 121 rqnfsrclclqcpdssltlpwpssprpleatpqppllllllpvglllaaawclh 180
 QY 207 WQTRRTTPRGEGQVPPVPSQDILLVEH 235
 Db 181 wqtrrttrpgrgeqvppvpsqdillveh 209

RESULT 11
 AAY69726
 ID AAY69726 standard; Protein; 209 AA.
 AC AAY69726;
 DT 05-JUL-2000 (first entry)
 DE Human flt3 mutein Q122R.
 DE
 KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200001823-A2.
 XX
 PD 13-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US14296.
 XX
 PR 02-JUL-1998; 98US-0109100.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Graddis TJ, McGrew JT;
 XX
 DR WPI; 2000-182115/16.
 XX
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122
 XX
 PS Claim 4; Page 88-89; 90pp; English.
 XX
 CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt-3
 CC ligands and comprises the Q122R mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
 CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.
 XX
 SQ Sequence 209 AA;
 Query Match 89.4%; Score 1110; DB 21; Length 209;
 Best Local Similarity 99.5%; Pred. No. 8.5e-97;

CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the L26 mutant polypeptide. The flt-3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt-3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX Sequence 209 AA;

Query Match 89.4%; Score 1110; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 8.5e-97;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 27 TDGCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLQDELCGLWRLVLAQRWMLR 86
DB 1 tqdcfsfqpissdfavkirelsdyllqdyptvasnlqdeecgglwrlvlaqrwmerl 60
QY 87 KTVAGSKMOGLLERNVTEHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVALKPWIT 146
DB 61 ktvtgskmgllervnteihfvtkcafpqppscrlrfvqtnisrlloetseqlvalkpwt 120
QY 147 RQNFRCLELQCPDSSSTLPPWSPRPLEATAPQPPPLLLLLPVGLLLAAAWCLH 206
DB 121 rqnfrsclclqcpdssstlppwsprrpleatpqppllllllpvglillaaawclh 180
QY 207 WQTRRRTPRPGEQVPPVPSQDILLVEH 235
DB 181 wqtrrrtrprgeqvppvpsqdillveh 209

RESULT 14
AY69722
ID AY69722 standard; Protein; 209 AA.
XX
AC AY69722;
XX
DT 05-JUL-2000 (first entry)
XX
DE Human flt-3 mutein H8Y.
XX
KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutein.

XX Homo sapiens.
OS Synthetic.
XX
PN WO200001823-A2.
XX
PD 13-JAN-2000.
XX
PF 25-JUN-1999; 99WO-US14296.
XX
PR 02-JUL-1998; 98US-0109100.
XX
PA (IMMUNEX) IMMUNEX CORP.
XX
PI Graddis TJ, McGrew JT,
XX
XX WPI; 2000-182115/16.

XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions,
PT contains amino acid substitutions at positions 8, 84, 118 or 122 .
XX
PS Claim 4; Page 81-82; 90pp; English.
XX
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AY69719) or mature (AY69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the H8Y mutant polypeptide. The flt-3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt-3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX Sequence 209 AA;

Query Match 89.2%; Score 1108; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 1.3e-96;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 27 TDGCSFQHSPISSDFAVKIRELSYLLQDYPTVTVASNLQDELCGLWRLVLAQRWMLR 86
DB 1 tqdcfsfqpissdfavkirelsdyllqdyptvasnlqdeecgglwrlvlaqrwmerl 60
QY 87 KTVAGSKMOGLLERNVTEHFVTKCAFQPPSPCLRFVQTNISRLLOETSEQLVALKPWIT 146
DB 61 ktvtgskmgllervnteihfvtkcafpqppscrlrfvqtnisrlloetseqlvalkpwt 120
QY 147 RQNFRCLELQCPDSSSTLPPWSPRPLEATAPQPPPLLLLLPVGLLLAAAWCLH 206
DB 121 rqnfrsclclqcpdssstlppwsprrpleatpqppllllllpvglillaaawclh 180
QY 207 WQTRRRTPRPGEQVPPVPSQDILLVEH 235
DB 181 wqtrrrtrprgeqvppvpsqdillveh 209

RESULT 15
AY69724
ID AY69724 standard; Protein; 209 AA.
XX
AC AY69724;
XX
DT 05-JUL-2000 (first entry)
XX
DE Human flt-3 mutein K84T.
XX
KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001823-A2.
XX
PD 13-JAN-2000.

XX 25-JUN-1999; 99WO-US14296.
 XX 02-JUL-1998; 98US-0109100.
 XX (IMMV) IMMUNEX CORP.
 XX Graddis TJ, McGrew JT;
 XX WPI; 2000-182115/16.
 XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 XX immune response stimulation or treatment of pathological conditions
 XX contains amino acid substitutions at positions 8, 84, 118 or 122 -
 XX
 XX Claim 4; Page 85-86; 90pp; English.
 XX
 XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 XX which exhibits increased or decreased biological activity relative to
 XX the full length wild type (AAV69719) or mature (AAV69720) flt3-L
 XX polypeptides. This sequence represents an example of the novel flt-3
 XX ligands and comprises the K84T mutant polypeptide. The flt3-L protein
 XX binds cell surface tyrosine kinase receptors and regulate growth and
 XX differentiation of hematopoietic progenitor cells. The flt3-L protein can
 XX be used to induce cellular expansion (especially in vivo) or
 XX differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 XX cells, especially in the presence of growth factors such as interleukins,
 XX colony stimulating factors or protein kinases. The protein can also
 XX modulate, augment or enhance a patient's immune response and can be used
 XX to treat an immune disorder (e.g. allergy, autoimmunity or
 XX immunosuppression). The protein may be used to treat a pathological
 XX condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 XX small cell lung, testicular or ovarian cancer, lymphoma, multiple
 XX myeloma, neuroblastoma or acute leukemia.
 XX
 XX Sequence 209 AA;

Query Match 89.2%; Score 1108; DB 21; Length 209;
 Best Local Similarity 99.5%; Pred. No. 1.3e-96;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELGGLWRLVLAQRMERL 86
 Db 1 tgcdfqhspsissdfavkirelsydlldqypvtvasnlqdeelogglwrlvlaqrwmerl 60
 Qy 87 KTVAGSKMOGLLEVRNTEIHFVTKAFOPPPSCLEFVOTNISRLLOETSEQLVALKPWIT 146
 Db 61 ktvagskmgqllervnteihvttcafpqppscrlfvqtnsrllqetseqivalkpwit 120
 Qy 147 RQNFSCLELQCPDSSTLPPWPSPRPLEATAPAPQPLLLLLPVGLLLAAACLIH 206
 Db 121 rqnfsarclclqcdsdtlppwpaprpleataptapqppllllllpvlllalaawclh 180
 Qy 207 WQTRRRTPRGEQVPPVPSQDILLVEH 235
 Db 181 wqtrrrtprrgeqvppvpsqdillveh.209

Search completed: April 1, 2002, 06:18:09
 Job time: 255 sec

Access DB# 63508**SEARCH REQUEST FORM**

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Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

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Searcher: <u>Jan</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>4498</u>	AA Sequence (#) <input checked="" type="checkbox"/> _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>4/1/02</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>4/1/02</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/> _____
Clerical Prep Time: <u>10</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>60</u>	Other _____	Other (specify) _____

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OM protein - protein search, using sw model

Run on: April 1, 2002, 06:13:54 ; Search time 68.03 seconds
(without alignments)
263.134 Million cell updates/sec

Title: US-08-162-407-6
Perfect score: 1242
Sequence: 1 MTVLAPAWSPTTYLLLLLLL.....RPGQVPPVPQDILLVEH 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	235	2 I38440	flt3 ligand - huma
2	864.5	69.6	245	2 S43293	FLT3/FLK2 ligand (
3	834	67.1	178	2 I39076	Flt3 ligand altern
4	768.5	61.9	231	2 A49265	flt3/flk-2 ligand
5	605.5	48.8	220	2 S43291	FLT3/FLK2 ligand (
6	605.5	48.8	220	2 I38343	flt3 ligand isofo
7	93	7.5	1217	2 T22672	hypothetical prote
8	92	7.4	661	1 T3BE12	74K alpha trans-in
9	89.5	7.2	474	2 T19543	hypothetical prote
10	89	7.2	387	2 I48201	adhalin - golden h
11	89	7.2	793	1 S60735	splicing factor SF
12	88.5	7.1	1386	2 T00257	hypothetical prote
13	88	7.1	753	2 J00532	OP protein - Kenne
14	87.5	7.0	479	1 A32290	protein-tyrosine-p
15	87	7.0	910	2 A53137	tyrosine kinase re
16	86.5	7.0	590	2 A40437	glutamic acid-rich
17	86	6.9	299	2 T17832	hypothetical prote
18	86	6.9	485	2 A33647	hypothetical prote
19	86	6.9	746	2 T28004	sulfated surface g
20	85	6.8	366	2 A37374	hypothetical prote
21	84	6.8	263	2 T03162	Fc gamma (IgG) rec
22	84	6.8	757	2 A39283	segment protein 6
23	83.5	6.7	199	2 E75630	gamma-glutamyl car
24	83.5	6.7	530	2 A45690	hypothetical prote
25	83	6.7	1509	2 T19486	transactivator EBN
26	82.5	6.6	418	2 T19800	hypothetical prote
27	82.5	6.6	426	2 I36948	Ig epsilon-chain
28	82.5	6.6	512	2 D40829	activin receptor 1
29	82.5	6.6	513	2 J01484	activin receptor p

30	82	6.6	106	2 T06479	proline/leucine-ri
31	82	6.6	854	2 T23837	hypothetical prote
32	81.5	6.6	485	2 C75460	hypothetical prote
33	81.5	6.6	488	2 S13423	stromelysin 3 (EC
34	81.5	6.6	958	2 T13593	hypothetical prote
35	81.5	6.6	1119	2 T50995	related to cytoske
36	81	6.5	196	2 B48232	cysteine-rich exte
37	81	6.5	209	2 A48232	cysteine-rich exte
38	81	6.5	388	2 S15591	probable transposa
39	81	6.5	428	1 EHHU	Ig epsilon chain C
40	80.5	6.5	636	2 JW0047	class I cyto kinase
41	80.5	6.5	1176	2 T49482	hypothetical prote
42	80.5	6.5	1305	2 T13592	hypothetical prote
43	80.5	6.5	1402	2 T46707	translocation initia
44	80	6.4	398	2 T52311	isopenicillin N ep
45	80	6.4	434	2 S74706	(S)-2-hydroxy-acid

ALIGNMENTS

RESULT 1

I38440
flt3 ligand - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
C:Accession: I38440; I39075; S43292
R:Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Down
Blood 83, 2795-2801, 1994
A:Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor f
A:Reference number: I38440; MUID:94235842,
A:Accession: I38440
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-235 <RES>
A:Cross-references: EMBL:U03858; NID:9494978; PIDN:AAAL9825:1; PID:9494979
R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1163-1172, 1995
A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581
A:Accession: I39075
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-235 <RE2>
A:Cross-references: EMBL:U29874; NID:g1072036; PIDN:AAA90949.1; PID:g1072037
R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.
felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotni
Nature 368, 643-648, 1994
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopo
A:Reference number: S43290; MUID:94195428
A:Accession: S43292
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-71, 'A', 73-235 <HAN>
A:Cross-references: GB:U04806; NID:9483844; PIDN:AAAL17999.1; PID:9483845
A:Note: the authors translated the codon AGT for residue 25 as Met
C:Genetics:
A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3

Query Match 100.0%; Score 1242; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.8e-99;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYDVLQDYPVTY 60
DB	1	MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYDVLQDYPVTY 60
QY	61	ASNLQDEELCGGLRWLRVLAQWRMERLKTAVAGSKMOGLLERVNTIEHVTKCAFPSPSCL 120
DB	61	ASNLQDEELCGGLRWLRVLAQWRMERLKTAVAGSKMOGLLERVNTIEHVTKCAFPSPSCL 120
QY	121	RFVQTNISRLQETSETSEQLVALKPWITRQNFSCRLELCQCPDSSTLPPPPSPRPLEATPT 180

Db 121 RFVQTNISRLQETSEQLVAKPWITRQNFSCLELQCPDSTLPPWSPRPLEATPT 180
 QY 181 APQPLLLLLLPVGLLLAAWCLHWQTRRTRPRGQVPPVSPQDLLLLVEH 235
 Db 181 APQPLLLLLLPVGLLLAAWCLHWQTRRTRPRGQVPPVSPQDLLLLVEH 235
 RESULT 2
 S43293
 FLT3/FLK2 ligand (clone S109) - human
 C:Species: Homo sapiens (man)
 C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
 C:Accession: S43293
 R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kiehl, A.; Muench, M.; Kellner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A. Nature 368, 643-648, 1994
 A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic cells
 A:Reference number: S43290; MUID:94195428
 A:Accession: S43293
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-245 <HAN>
 A>Note: the authors translated the codon AGT for residue 25 as Met

Query Match 69.6%; Score 864.5; DB 2; Length 245;
 Best Local Similarity 73.0%; Pred. No. 8.5e-67;
 Matches 176; Conservative 7; Mismatches 27; Indels 31; Gaps 3;

QY 1 MTVLAPAWSPPTLYLLSSLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
 Db 1 MTVLAPAWSPPTLYLLSSLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
 QY 61 ASNLQDEELCGGLRWLRVLAQRWMLKTVAGSKMGLLERNVTEHFVTKCAFQPPPSCL 120
 Db 61 ASNLQDEELCGGLRWLRVLAQRWMLKTVAGSKMGLLERNVTEHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVAKPWITRQNFSCLELQCPDSTLPPWSPRPLEATPT 180
 Db 121 RFVQTNISRLQETSEQLVAKPWITRQNFSCLELQCPDSTLPPWSPRPLEATPT 180
 QY 181 APQP-----PLLLLLLPVGLLLAAWCLHWQTRRTRPRGQVPPVSP 227
 Db 178 WPRPHGEDTENHRESP-----ARGCIATWQTKLARGSLPWAPLIPSP 222
 QY 228 Q 228
 Db 223 E 223

RESULT 3
 I39076
 FLT3 ligand alternatively spliced isoform - human
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
 C:Accession: I39076
 R:Lyman, S.D.; Stocking, K.; Davidson, B.; Fletcher, F.; Johnson, L.; Escobar, S. Oncogene 11, 1165-1172, 1995
 A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
 A:Reference number: I39075; MUID:96032581
 A:Accession: I39076
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-178 <RES>
 A:Cross-references: EMBL:U29874; NID:g1072036; PIDN:AAA90950.1; PID:g1072038
 C:Genetics:
 A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1

Query Match 67.1%; Score 834; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 2.4e-64;
 Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPPTLYLLSSLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
 Db 1 MTVLAPAWSPPTLYLLSSLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
 QY 61 ASNLQDEELCGGLRWLRVLAQRWMLKTVAGSKMGLLERNVTEHFVTKCAFQPPPSCL 120
 Db 61 ASNLQDEELCGGLRWLRVLAQRWMLKTVAGSKMGLLERNVTEHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVAKPWITRQNFSCLELQCP 160
 Db 121 RFVQTNISRLQETSEQLVAKPWITRQNFSCLELQCP 160
 RESULT 4
 A49265
 flt3/flk-2 ligand precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
 C:Accession: A49265; I49347; I49346; S43290
 R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Hollt, D.; Williams, D.E.; Beckmann, M.P. Cell 75, 1157-1167, 1993
 A:Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a cDNA
 A:Reference number: A49265; MUID:94084791
 A:Accession: A49265
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-231 <LYM>
 A:Cross-references: GB:L23636; NID:9439441; PIDN:AAA9436.1; PID:g439442
 R:Lyman, S.D.; Stocking, K.; Davidson, B.; Fletcher, F.; Johnson, L.; Escobar, S. Oncogene 11, 1165-1172, 1995
 A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
 A:Reference number: I39075; MUID:96032581
 A:Accession: I49347
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-163, 'G', '165', 'HYAG' <RES>
 A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041
 A:Accession: I49346
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-197, 'L', 198-231 <RE2>
 A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040
 R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kiehl, A.; Muench, M.; Kellner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A. Nature 368, 643-648, 1994
 A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic cells
 A:Reference number: S43290; MUID:94195428
 A:Accession: S43290
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-197, 'L', 198-231 <HAN>
 A:Experimental source: clone T110
 A>Note: the sequence from Fig. 2c is inconsistent with that from Fig. 2a in having 4-
 C:Genetics:
 A:Introns: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3
 C:Keywords: transmembrane protein

Query Match 61.9%; Score 768.5; DB 2; Length 231;
 Best Local Similarity 70.3%; Pred. No. 1.3e-58;
 Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MTVLAPAWSPPTLYLLSSLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 59
 Db 1 MTVLAPAWSPNSLLLLLLLSPCLRGTPDCYFESHSPISNFVKVFKRELTHLLKDYPT 60
 QY 60 VASNLQDEELCGGLRWLRVLAQRWMLKTVAGSKMGLLERNVTEHFVTKCAFQPPPSCL 119
 Db 61 VAVNLQDEKCHKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTVTEHFVTSCTFQPLPEC 120
 QY 120 LRFVQTNISRLQETSEQLVAKPWITR--QNFSCLELQCPDSTLPPWSPRPLEAT 177

Db 121 LRFVOTNISHLLKDTCTQLLAKPCIGKACQNFSCLEVCQCPDSSTLLPFRSPALEAT 180
 QY 178 APTAPQPP--LILLLLLPVGLLLAAAWCLHWQRTRRRTFRGEQVPPVPSP 227
 Db 181 ELPEPRPQLLLLLLLPLTLVLLAAWGLRQWRARR--GELHPGVPLP 228

RESULT 5

S43291
 FLT3/FLK2 ligand (clone T118) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
 C:Accession: S43291
 R:Hannum, C.; Cuilepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kiehl, A.; Muench, M.; Kelnner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnick, A. Nature 368, 643-648, 1994
 A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic cells
 A:Reference number: S43290; MUID:94195428
 A:Accession: S43291
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-220 <HAN>

Query Match 48.8%; Score 606.5; DB 2; Length 220;
 Best Local Similarity 61.5%; Pred. No. 9.4e-45;
 Matches 134; Conservative 18; Mismatches 43; Indels 23; Gaps 5;

QY 1 MTVLAPAWSP-TYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 59
 Db 1 MTVLAPAWSPNSULLLLLSPLCRGTDCYFSHSPISSNFVKFRELTDHLKDYPT 60

QY 60 VASNLQDEELCGGLRLVLAQRWMLKTVAGSKMQGLLRVNTFHFVTKCAFQPPSPC 119
 Db 61 VAVNLQDEKCKALWSLFLAQRWTEQKTVAGSKMQGLLDVNTFHFVTSCTFQPLPEC 120

QY 120 LRFVOTNISHLLQETSEQLVALKPWITR--ONFSRCLELQCPDSSTLPPWSPRP---- 173
 Db 121 LRFVOTNISHLLKDTCTQLLAKPCIGKACQNFSCLEVCQCPGNG-----GPRHQHG 174

QY 174 ---LEATAPAPQPPILL-----LLLLPVGLLLAA 201
 Db 175 ATRLTATALLTVCPLLLPLVGTSHMFFLPFLSLSS 212

RESULT 6

I58343
 flt3 ligand isoform 5H - mouse
 C:Species: Mus sp. (mouse)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I58343
 R:Lyman, S.D.; James, L.; Escobar, S.; Downey, H.; de Vries, P.; Brasel, K.; Stocking, K. Oncogene 10, 149-157, 1995
 A:Title: Identification of soluble and membrane-bound isoforms of the murine flt3 ligand
 A:Reference number: I58343; MUID:95124710
 A:Accession: I58343
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-220 <RES>
 A:Cross-references: GB:S76459; NID:9913479; PIDN:AAB33069.1; PID:9913480

Query Match 48.8%; Score 606.5; DB 2; Length 220;
 Best Local Similarity 61.5%; Pred. No. 9.4e-45;
 Matches 134; Conservative 18; Mismatches 43; Indels 23; Gaps 5;

QY 1 MTVLAPAWSP-TYLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 59
 Db 1 MTVLAPAWSPNSULLLLLSPLCRGTDCYFSHSPISSNFVKFRELTDHLKDYPT 60

QY 60 VASNLQDEELCGGLRLVLAQRWMLKTVAGSKMQGLLRVNTFHFVTKCAFQPPSPC 119
 Db 61 VAVNLQDEKCKALWSLFLAQRWTEQKTVAGSKMQGLLDVNTFHFVTSCTFQPLPEC 120

Db 61 VAVNLQDEKCKALWSLFLAQRWIEQLKTVAGSKMQGLLEDVNTFHFVTSCTFQPLPEC 120
 QY 120 LRFVOTNISHLLQETSEQLVALKPWITR--ONFSRCLELQCPDSSTLPPWSPRP---- 173
 Db 121 LRFVOTNISHLLKDTCTQLLAKPCIGKACQNFSCLEVCQCPGNG-----GPRHQHG 174
 QY 174 ---LEATAPAPQPPILL-----LLLLPVGLLLAA 201
 Db 175 ATRLTATALLTVCPLLLPLVGTSHMFFLPFLSLSS 212

RESULT 7

T22672
 hypothetical protein F54F12.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T22672
 R:Barlow, K. W
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19597
 A:Accession: T22672
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1217 <WIL>
 A:Cross-references: EMBL:Z81548; NID:e1062020; PIDN:CAB04464.1; GSPDB:GN00021; CESP:F412
 A:Experimental source: clone F54F12
 C:Genetics:
 A:Gene: CESP:F54F12.1
 A:Map position: 3
 A:Introns: 742/2; 826/1; 884/2; 922/3; 972/1; 1024/2; 1102/1

Query Match 7.5%; Score 93; DB 2; Length 1217;
 Best Local Similarity 23.6%; Pred. No. 6.2;
 Matches 38; Conservative 33; Mismatches 68; Indels 22; Gaps 6;

QY 83 MERLKTAVAGSKMQL---LERVNTFHFVTKCAFQPPSPCLRFVQTNISRLQETSEQLV 139
 Db 627 MDVAVKAVDGTYSVIDALEKLSLMDLDFQKFKFAPATLKAMDL----FFASVASNLA 682

QY 140 ALKPWITRQNFSCLELQCPDSSTL---PPWSPRPLEATAPAP-----QPPLLLLLL 191
 Db 683 ALRQPTTSDPTAAPVPIPNKGSINGNPSPSPPLPPVASSTPAATPESNMILLYII 742

QY 192 LPVGLLLAA-----AWCLHWQRTRRTPRGEQVPPVPSP 227
 Db 743 GAVGGLLVVAITGVILFEVFFQKKKKEDKDD--PPAPLP 781

RESULT 8

TNBE12
 74K alpha trans-inducing protein - human herpesvirus 3
 C:Species: human herpesvirus 3, varicella-zoster virus
 C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999
 C:Accession: C27342
 R:Davidson, A.J.; Scott, J.E.
 J. gen. Virol. 67, 1759-1816, 1986
 A:Title: The complete DNA sequence of varicella-zoster virus.
 A:Reference number: A27345; MUID:86306657
 A:Accession: C27342
 A:Molecule type: DNA
 A:Residues: 1-661 <DAV>
 A:Cross-references: EMBL:X04370; NID:g59989; PIDN:CAA27895.1; PID:g60001
 C:Genetics:
 A:Gene: 12
 C:Superfamily: herpesvirus 77K alpha trans-inducing protein
 C:Keywords: trans-inducing protein; transcription regulation

Query Match 7.4%; Score 92; DB 1; Length 661;
 Best Local Similarity 26.6%; Pred. No. 3.8;
 Matches 61; Conservative 29; Mismatches 103; Indels 36; Gaps 11;

```

19  LLSSGLSGTDCS-----FQHSPTSSDFAVKI--RELSDYLLQDYPVTVASNLQDEELCG- 71
Db 79  LTFPVQLQSTHERHVVLLGLHHNNVPESLVVSYSCMSNDVHDGFQMYMETIQRCILDDLLKLSGD 138
QY 72  GLWRLVLAQRMERLKTVAGSKMOGLLRVN-----TEHFVTKCAFOP---PPSCLRFV 123
Db 139  GLW-WYENTYQWLYKYTGAEPVTVSEKVNKSKSTVLLFSSVVANKPISRHPFKSVKI 197
QY 124  QTNISRLQETSQVLVAKPWITRONFHSRCLELQCPQDSSTLPPWSP-RPLEATAPTAP 182
Db 198  NSDYRGICQELREALGAVOKYM---YFMR-----PDDPTNPSPDTRIRVQEIYAATAT 247
QY 183  QPFLLLLLLPVGLLLLAACWLHMQTRRRTPRCEQVPPVPSQDLL 231
Db 248  GYGWMLFQDVVD-----ARVCRHLKQFRRIRGRASV-----IPDPLL 287

RESULT      9
T19543
hypothetical protein C28D4.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T19543
R:McMurray, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19139
A/Accession: T19543
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-474 CWIL>
A/Cross-references: EMBL:Z82259; PIDN:CAB05129.1; GSPDB:GNO0022; CESP:C28D4
A/Experimental source: clone C28D4
C/Genetics:
A:Gene: CESP:C28D4.2
A/Map position: 4
A/Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/2

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Query Match	7.2%	Score 89.5;	DB 2;	Length 474;	
Best Local Similarity	24.1%;	Pred. No. 4.2;			
Matches	59;	Conservative	29;	Mismatches 82; Indels 75; Gaps 15;	
QY	27	TQDC-----	SFQHS-PISSDFAVKIREL-SDYLLQDYPVTVASNLQDEELCGGLWRL	76	
Db	65	TTDCVDLKKVFSKFDSSAPISGEILFRARFLCAKYL-----	GGAWRK	106	
QY	77	VLAQRMMERLKTVAGSKWOGLLERNVTEIHFTVKCAQPPPSCLR-FVQTNISRLQET-	134		
Db	107	VKIEEF--RIRATGG-MSNLLFVLVPAH-LTPIQMEPEKALLRVHCQSDIDGLSES	162		
QY	135	-----	SEOLVAKPWITTRNFSCLELOQ-----	QPDSSITLPPWSPR--PLBATA	178
Db	163	VFTLLSERNLGPMGVFGGRFEQFTPSRALQCLEISKGLSLIAPIVARVITLDAPI	222		
QY	179	PTAPQPLLLLLLPVGLLLLAANWCWHWORTTRTP-----	RPGE-----	QVPPVPSPQD	229
Db	223	PKEPQ-----	TLQTAQWLERF-----	KKTPAGERPIEMLYTAQKVPSDYPST	266
QY	230	LLIVE	234		
Db	267	ITVAQ	271		

RESULT 10
I48201
adhalin - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Jun-2000
C:Accession: I48201
R:Roberts, S.L.; Campbell, K.P.
FEBS Lett. 364, 245-249, 1995
A:Title: Adhalin mRNA and cDNA sequence are normal in the cardiomyopathic hamster.
A:Reference number: I48201; PMID:95278335

A;Accession: I48201
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-387 <RES>
A;Cross-references: EMBL:U21677; NID:g726481; PID:g726482
C;Superfamily: mouse adhalin

Query Match	7.2%	Score 89;	DB 2;	Length 387;
Best Local Similarity	23.4%;	Pred. No. 3.7;		
Matches 71;	Conservative 26;	Mismatches 97;	Indels 110;	Gaps 14;

QY	11	TTYLLLLLLSSGLSTQDCSFQHSPISSFAWKIRELSDYLLQDYPVTVASNLQDEELC	70
Db	115	TTTQRLLLLT-----EDPEGRLLPYQAEFLVRSHDVEVL-----PSTPANRFL--TAL	161
QY	71	GGWLRL-----VLAQRHMERLKTVAGSKMOGLLERVNTETHFVT-----K	110
Db	162	GGWLWELGELQLLNITSALDRGGRVPILPIEGRKEGVYIKVGSATPFSTCLKMVASPDSYAR	221
QY	111	CAFQPPP--SC-----LRFVQNTISRLQETSEOLVALKPWITRQNFSCRLELOCOPD	161
Db	222	CAQGQPLLSCYDSLAPHFRVDCNLSLVDKSVPELID-----EVPTPGD	266
QY	162	SSTLPPWPSPRPLEAT-----APTAQPPLLLLLLPVGLLLALAAWC-----	204
Db	267	GILEHDPFCPPTEATGRDFLADALVTLLVPLLVALLL---TLLLAYIMCCRREGQLKRD	323
QY	205	-----LHWQRTTRRRTPRP-----GEQVPP--VPSPO--DLL	231
Db	324	MATSDIQMVHCHTIGHNTEELRQMAARREVPRLSTLPMFNVRTGERLPRVDSAQVPLI	383
QY	232	LVEH 235	
Db	384	LDCH 387	

RESULT 11
S60735
splicing factor SF3a 120K chain - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: S60735; S60733
R:Kraemer, A.; Mulhauser, F.; Wersig, C.; Groening, K.; Bilbe, G.
RNA 1, 260-272, 1995
A:Title: Mammalian splicing factor SF3a120 represents a new member of the SURP family
A:Reference number: S60733; MUID: 96079958
A:Accession: S60735
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-793 <KRA>
A:Cross-references: EMBL:X85237; NID:g899297; PIDN:CAA59494.1; PID:g899298
A:Accession: S60733
A:Molecule type: protein
A:Residues: 51-62;82-94;270-275;397-414;448-463 <KRA2>
C:Genetics:
A:Gene: GDB:SF3A120; PRP21; SAP114
A:Cross-references: GDB:9955873
A:Map position: 22q12.1-22qter
C:Superfamily: human splicing factor SF3a 120K chain; ubiquitin homology
C:Keywords: pre-mRNA splicing
F:714-790/Domain: ubiquitin homology <UBH>

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Query Match          7.2%; Score 89; DB 1; Length 793;
Best Local Similarity 22.3%; Pred. NO. 8.4;
Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

QY 4 LAPAWSTTYLLLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPTVTASN 63
  ||| ||| ||| ||| |||
DB 401 LPPAPAPDEYLV-----SPITGE-----KI-----PASK 424

QY 64 LODEELCGGLWRVLVLAQRNWE-RLKTV-----AGSKMQGLLERYVNTETIHF 107

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Db 425 MOEHRIG-----LDPRWLEQRDRSIREKQSDDEVYAPGLDISSKOLAER-RTDIFG 478
 Qy 108 VTKCA-----FQPPSSCLRF-----VOTNISRLQETSEQLVAKPW 145
 Db 479 VEETAIGKIGEEETOKPEKVTWGHSGSMARTQQAQANIT--LQEQEALHKAGLV 536
 Qy 146 ----TRQNF--SRCLELOCP-----DSSTLP-----PPWSRPLEAT-----APT 180
 Db 537 PEDDTKERIGSKNEIQOQPPPPSATNIPSSAPITSPVPRPTMPVPRITVVSAVPV 596
 Qy 181 APOPLLILLPVLGILLAAWCLHWQTR-----RRTPRGQVPP-----VPSP 227
 Db 597 MPRPPMASVVRPPGSIAPMPPIIHAPRINVVMPSPAPPIAPRPPMIVPTAFVPAP 656
 RESULT 12
 T00257
 hypothetical protein KIAA0476 - human
 C:Species: Homo sapiens (man)
 C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
 C:Accession: T00257
 DNA Res. 4: 345-349, 1997
 R:Seiki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
 A>Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human
 A:Reference number: 214085; MUID:98116662
 A:Accession: T00257
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1386 <SEK>
 A:Cross-references: EMBL:AB007945; NID:g3413913; PIDN:BAA32321.1; PID:g3413914
 A:Experimental source: brain
 C:Genetics:
 A:Note: KIAA0476

Query Match 7.18; Score 88.5; DB 2: Length 1386;
 Best Local Similarity 23.18; Pred. No. 17;
 Matches 53; Conservative 28; Mismatches 85; Indels 63; Gaps 12;
 Qy 21 SSGLSGTQDCSFQHSPISSDFAVIRELSVLLQDYPVTVASNLQDELC---GGLWRL 76
 Db 1104 SAGASGSKDAPVCGP-----GVLSDRRUCLA--LDEPOLCNGHMGASRR 1148
 Qy 77 VLAQRWMLRTVAGSKMGLLERNTEIFVTKCAFQPPSPCLRFVOTNISRLQETSE 136
 Db 1149 VESGAWAYLSPLVRKELESVENEGSEV-----LALPELPSAHPPIIWNLLWYFQRL-- 1201
 Qy 137 OLVALKPWITRQNSRCLELOCP--PDSSTLPPW--SPRPLEA-----TAPTAPQPP 185
 Db 1202 RUPSILPGLVLAS-----CDGSPSHSQAPSPWLTDPASVQVRLLDVLTDPDPSNCP 1253
 Qy 186 LLLILLPVLGILLAAWCLHWQTRRRTPRGQVPPVPSQDLLLYE 234
 Db 1254 LVYL-----WRVHSQ--IPORVWMPG-----VVPASLSLALLE 1284

RESULT 13
 JQ0532
 OP protein - Kennedy's yellow mosaic virus
 C:Species: Kennedy's yellow mosaic virus
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999
 C:Accession: JQ0532
 R:Ding, S.; Keese, P.; Gibbs, A.
 J. Gen. Virol. 71, 925-931, 1990
 A>Title: The nucleotide sequence of the genomic RNA of Kennedy's yellow mosaic tymovirus-
 A:Reference number: JQ0532; MUID:90218040
 A:Accession: JQ0532
 A:Molecule type: mRNA
 A:Residues: 1-753 <DIN>
 A:Cross-references: GB:D00637; NID:g221969; PIDN:BAA00531.1; PID:d1000986; PID:g221970
 A:Experimental source: strain Jervis Bay isolate

Query Match 7.18; Score 88; DB 2: Length 753;
 Best Local Similarity 22.38; Pred. No. 9.6;
 Matches 41; Conservative 19; Mismatches 58; Indels 66; Gaps 7;
 Qy 100 RVNTEIFVTKCAFQPPSPCLRF-----VQTNIS-----RLQETSEQLVAKPWITR 147
 Db 420 RLSTQPPSPQTSSTSSPPSPRTDASCIQIPLASPPSKREKSLPHFSHQ-----PPSHSK 475
 Qy 148 QNFSR-----CLEQOCQDSSTLPPSPRPLEATAPAPQPLLLLLLP----- 193
 Db 476 RNLRRHSALPLLPIHPTKTQHPAVQP--TAGTPHPPTTKIPLHPPKSOERHSP 533
 Qy 194 -----VGLLLAAANCLHWQTRRRTPRGQVPPVPS 226
 Db 534 PDVFDHCQSPSTSHVGYRLLGSGISLPFKLAFN-----RRRSPNPARHLPPPPP 586
 Qy 227 PQDLW230
 Db 587 PRKL 590

RESULT 14
 A32290
 protein-tyrosine-phosphatase (EC 3.1.3.48) cdc25 homolog string - fruit fly (Drosophila)
 C:Species: Drosophila melanogaster
 C:Date: 05-Oct-1989 #sequence_revision 25-Apr-1997 #text_change 11-Jun-1999
 C:Accession: A32290; SI2008
 R:Edgar, B.A.; O'Farrell, P.H.
 Cell 57, 177-187, 1989
 A>Title: Genetic control of cell division patterns in the Drosophila embryo.
 A:Reference number: A32290; MUID:89195217
 A:Accession: A32290
 A:Molecule type: mRNA
 A:Residues: 1-479 <EDG>
 A:Cross-references: GB:M24909; NID:g158507; PIDN:AAA28916.1; PID:g158508
 R:Jimenez, J.; Alpheg, L.; Nurse, P.; Glover, D.M.
 EMBO J. 9, 3565-3571, 1990
 A>Title: Complementation of fission yeast cdc2(ts) and cdc25(ts) mutants identifies
 A:Reference number: SI2008; MUID:91006056
 A:Accession: SI2008
 A:Molecule type: mRNA
 A:Residues: 1-227 'A', 229-479 <JIM>
 A:Cross-references: EMBL:X57495; NID:g7706; PIDN:CAA40732.1; PID:g7707
 C:Genetics:
 A:Gene: FlyBase:stg
 A:Cross-references: FlyBase:FBgn0003525
 C:Function:
 A:Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine
 A:Pathway: Initiation of mitosis
 A:Note: cdc25 activates the cdc2 protein kinase by dephosphorylating it
 C:Superfamily: protein-tyrosine-phosphatase string; cdc25-type protein-tyrosine-phosphatase
 C:Keywords: cell cycle control; mitosis; phosphoprotein; phosphoric monoester hydrolase
 F:252-456/Domain: cdc25-type protein-tyrosine-phosphatase homology <PPP>
 F:379/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:385/Binding site: substrate phosphate (Arg) #status predicted

Query Match 7.08; Score 87.5; DB 1: Length 479;
 Best Local Similarity 22.98; Pred. No. 6.3;
 Matches 56; Conservative 34; Mismatches 76; Indels 79; Gaps 14;
 Qy 1 MTVLAPANSPYYLL--LLLSLSCSLSTQDCSFQHSPISSDFAVIRELSYLLQDYP 57
 Db 72 MGLLSPESQFQIVRQPKILPAMGVSS-----DHTPARS-FRI-FNSLSS-----T 117
 Qy 58 VTVASNLODEELCGGLWRLVLAQRWMLRTVAGSKMGLLERNTEIFVTKCAFQPP 117
 Db 118 CSMESMDE-----YMEFEMESQSQ-----QTALGF-----P 146
 Qy 118 SCLRFVQTNISRLQETSEQLVAKP--WITRQNFSCRLEL-QCQPDSSSTLPPWSPRP 173
 Db 147 SGLN-----SLISQIKQPAKSPAGLSMRPVSRRCLSWESTNSTTTTPPKTPE- 199

Qy 174 LEATAPTA---PQPLLPLLLLVGLLLAAAWCLHWQTRRRTPRGEQVPPVPSQDL 230
|||
Db 200 ---TARDCFKRPEPP-----ASANGSPIQSKRHCATVEKENCAPSPLSQ 242
Qy 231 LLVEH 235
Db 243 VTISH 247

RESULT 15

A53137
tyrosine kinase receptor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C/Accession: A53137
R/Sanchez, M.P.; Tapley, P.; Saint, S.S.; He, B.; Pulido, D.; Barbacid, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 1819-1823, 1994
A/Title: Multiple tyrosine protein kinases in rat hippocampal neurons: isolation of Ptk-
A/Reference number: A53137; MUID:94173920
A/Accession: A53137
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-910 <RES>
A/Cross-references: GB:L26525; NID:g432480; PIDN:AAA21089.1; PID:g432481
C/Genetics:
A/Gene: Ptk-3
C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino-ter
C/Keywords: Atp
F:31-186/Domain: discoidin I amino-terminal homology <DN1>
F:605-909/Domain: protein kinase homology <KIN>
F:613-621/Region: protein kinase ATP-binding motif

Query Match 7.0% Score 87; DB 2; Length 910;
Best Local Similarity 24.5%; Pred. No. 15;
Matches 38; Conservative 12; Mismatches 35; Indels 70; Gaps 9;
Qy 143 PWITRQNFRCLEQCQPDSTLPP-PW---SPRPLEATA----PTAFQP----- 184
|||
Db 356 PWLLFSEISFISDV-VNDSSTPTPPAPWPPGPPPTNFSLELEPRGQOPVAKAGSPTA 414
Qy 185 -----PLLLLLLVGLLLAAAWCLHWQTRRR-----TTRR-----T 214
Db 415 ILIGCLVAIIILLIIIALML-----WRLHWRLSKAERRVLEELAVHLSVPGDTILIN 470
Qy 215 PRGGEQVPP-----VPSQDILL 232
Db 471 NRPGPREPPYQEPFRGTPTHSAPCVNGSALLL 505

Search completed: April 1, 2002, 06:15:21
Job time: 87 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 1, 2002, 06:16:39 ; Search time 68.97 Seconds
(without alignments)
124.927 Million cell updates/sec

Title: US-08-162-407-6

Sequence: 1 MTVLAPAWSPTTLLLLLLL.....RPGQVPPVSPQDILLIVEH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	235	1 FL3L_HUMAN	P49771 homo sapien
2	768	61.8	232	1 FL3L_MOUSE	P49772 mus musculus
3	92	7.4	661	1 AT12_VZVD	P09264 varicella-z
4	89.5	7.2	941	1 GBR2_HUMAN	O75899 homo sapien
5	89	7.2	387	1 SGCA_MESAU	O64255 mesocricetu
6	89	7.2	793	1 S3A1_HUMAN	O15459 homo sapien
7	87.5	7.0	415	1 TNRC_MOUSE	P50284 mus musculus
8	87.5	7.0	479	1 MP1P_DROME	P20483 drosophila
9	87	7.0	910	1 DDRI1_MOUSE	Q63474 rattus norv
10	86.5	7.0	1394	1 CNG4_BOVIN	Q03146 mus musculus
11	86	6.9	485	1 SSGP_VOLCA	Q28181 bos taurus
12	85	6.8	282	1 ATF5_HUMAN	P21997 volvox cart
13	85	6.8	365	1 FCGN_RAT	O972d1 homo sapien
14	84	6.8	582	1 MNT_HUMAN	P13599 rattus norv
15	84	6.8	732	1 YF48_HUMAN	Q99583 homo sapien
16	83.5	6.7	671	1 T282_HUMAN	O9hcm4 homo sapien
17	83.5	6.7	758	1 VKGK_HUMAN	O9udv7 homo sapien
18	83	6.6	488	1 KM11_HUMAN	P38435 homo sapien
19	81.5	6.6	591	1 MNT_MOUSE	P24347 homo sapien
20	81.5	6.6	591	1 MNT_MOUSE	O08789 mus musculus
21	81.5	6.6	2124	1 Y192_HUMAN	Q93074 homo sapien
22	81	6.5	283	1 ATF5_MOUSE	O70191 mus musculus
23	81	6.5	387	1 SGCA_MOUSE	P82350 mus musculus
24	81	6.5	428	1 EPC_HUMAN	P01854 homo sapien
25	81	6.5	1248	1 DIAL_HUMAN	O60610 homo sapien
26	80.5	6.5	1402	1 IF4G_RABIT	P41110 oryctolagus
27	80	6.4	397	1 CEFD_STRCL	P18549 streptomyce
28	80	6.4	940	1 GBR2_RAT	O88871 rattus norv
29	80	6.4	1174	1 KPCL_COEHE	O42632 cochlilobu
30	80	6.4	1794	1 YAVI_SCHPO	Q40172 schizosacch
31	79	6.4	805	1 XGW6_YEAST	P53086 saccharomyc
32	78.5	6.3	251	1 HXB4_HUMAN	P17483 homo sapien
33	78.5	6.3	382	1 AVRE_RAT	P38445 rattus norv

34	78.5	6.3	387	1 SGCA_RABIT	Q28686 oryctolagus
35	78.5	6.3	913	1 DDRI1_HUMAN	Q08345 homo sapien
36	78.5	6.3	1180	1 AT12_HUMAN	Q9nq11 homo sapien
37	78	6.3	205	1 CYSR_SYNY3	Q55854 synechocyst
38	78	6.3	566	1 TS13_MOUSE	Q01755 mus musculus
39	77.5	6.2	1885	1 FAS2_CANAL	P43098 c fatty aci
40	77.5	6.2	2004	1 MOZ_HUMAN	Q92794 homo sapien
41	77	6.2	195	1 CORA_HPBVF	P29178 hepatitis b
42	77	6.2	316	1 CONC_HUMAN	P49918 homo sapien
43	77	6.2	367	1 MREC_ECOLI	P16926 escherichia
44	77	6.2	478	1 BM3B_HUMAN	P35107 homo sapien
45	77	6.2	742	1 PKWA_THECU	P49695 thermomonos

ALIGNMENTS

RESULT 1
FL3L_HUMAN
ID FL3L_HUMAN STANDARD; PRT; 235 AA.
AC P49771;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SL CYTOKINE PRECURSOR (FMS-RELATED TYROSINE KINASE 3 LIGAND) (FLT3
DE LGAND).
GN FLT3LG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:94195428; PubMed:8145851;
RA Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,
RA Bazar J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J.,
RA Duda G., Martina N., Peterson D., Menon S., Shanafelt A.,
RA Muench M., Kellner G., Namikawa R., Rennick D., Roncarolo M.G.,
RA Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.,
RT "Ligand for FLT3/Flk2 receptor tyrosine kinase regulates growth of
RT haematopoietic stem cells and is encoded by variant RNAs."
RL Nature 368:643-648(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE:94235842; PubMed:8180375;
RA Lyman S.D., James L., Johnson L., Brasel K., de Vries P.,
RA Escobar S.S., Downey H., Splett R.R., Beckmann M.P., McKenna H.J.,
RT "Cloning of the human homologue of the murine flt3 ligand: a growth
RT factor for early hematopoietic progenitor cells."
RL Blood 83:2795-2801(1994).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE:96032581; PubMed:7566977;
RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
RA Escobar S.S.;
RT "Structural analysis of human and murine flt3 ligand genomic loci."
Oncogene 11:1165-1172(1995).
CC -!- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
CC FACTORS AND INTERLEUKINS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. A SOLUBLE FORM
CC IS ALSO PRODUCED BY ALTERNATIVE SPLICING.
CC -!- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING.

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DR EMBL; U04806; AAA1999.1; -
 DR EMBL; U03858; AAA19825.1; -
 DR EMBL; U29874; AAA90949.1; -
 DR EMBL; U29874; AAA90950.1; -
 DR MIN; 600007; -
 KW Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 235
 FT DOMAIN 27 184
 FT TRANSMEM 27 205
 FT TRANSMEM 185 205
 FT DOMAIN 206 235
 FT CARBOHYD 126 126
 FT CARBOHYD 149 149
 FT VARSPLIC 161 178
 FT VARSPLIC 179 235
 FT CONFLICT 72 72
 FT SEQUENCE 235 AA; 26416 MW; 73B95BF693B4CECF CRC64;
 SQ
 Query Match 100.0%; Score 1242; DB 1; Length 235;
 Best Local Similarity 100.0%; Pred. No. 6.3e-98;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MTVLAPAWSPPTLYLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDPVTV 60
 Db 1 MTVLAPAWSPPTLYLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDPVTV 60
 Qy 61 ASNLQDELCGLRLVLAQRWMLKTVAGSKMGLLRYNTEHFYTKAFQPPPSCL 120
 Db 61 ASNLQDELCGLRLVLAQRWMLKTVAGSKMGLLRYNTEHFYTKAFQPPPSCL 120
 Qy 121 RVQTNISRLQETSEQLVALKPTWTRQNSRCLQLQCPDSSITLPPWSPRPLEATAPT 180
 Db 121 RVQTNISRLQETSEQLVALKPTWTRQNSRCLQLQCPDSSITLPPWSPRPLEATAPT 180
 Qy 181 AQPPPLLLLLPVGLLLLAAWCLHMQRTRRRPRGQVPPVPSQDILLVEH 235
 Db 181 AQPPPLLLLLPVGLLLLAAWCLHMQRTRRRPRGQVPPVPSQDILLVEH 235
 RESULT 2
 FL3L_MOUSE STANDARD; PRF; 232 AA.
 ID FL3L_MOUSE
 AC P49772;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE SL CYTOKINE PRECURSOR (FMS-RELATED TYROSINE KINASE 3 LIGAND) (FLT3
 DE LIGAND).
 DE FL3LG OR FLT3L.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94195428; PubMed=8145851;
 RA Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,
 RA Bazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J.,
 RA Duda G., Martina N., Peterson D., Menon S., Shanafelt A.,
 RA Muench M., Keiner G., Namikawa R., Rennick D., Roncarolo M.G.,
 RA Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.,
 RA "Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of
 RT haematopoietic stem cells and is encoded by variant RNAs.";
 RL Nature 368:643-648(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SJL/J;
 RX MEDLINE=94084791; PubMed=7505204;
 RA Lyman S.D., James L., Vandenbos T., Devries P., Brasel K.,
 RA Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J.,
 RA Spiett R.N., Fletcher F.A., Maraskovsky E., Farran H.,

RA Foxworthe D., Williams D.E., Beckmann M.P.;
 RT "Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase
 RT receptor: a proliferative factor for primitive hematopoietic cells.";
 RL Cell 75:1157-1167(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96032581; PubMed=7566977;
 RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
 RA Escobar S.;
 RT "Structural analysis of human and murine flt3 ligand genomic loci.";
 RL Oncogene 11:1165-1172(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95124710; PubMed=7824267;
 RA Lyman S.D., James L., Escobar S., Downey H., de Vries P.,
 RA Brasel K., Stocking K., Beckmann M.P., Copeland N.G.,
 RA Cleveland D.S.;
 RT "Identification of soluble and membrane-bound isoforms of the murine
 RT flt3 ligand generated by alternative splicing of mRNAs.";
 RL Oncogene 10:149-157(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX McClanahan T., Culpepper J., Campbell D., Wagner J.,
 RA Franz-Bacon K., Mattson J., Tsai S., Luh J., Guimares M.J.,
 RA Mattei M.-G., Rosnet O., Birnbaum D., Hannum C.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
 CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
 CC FACTORS AND INTERLEUKINS.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. A SOLUBLE FORM
 CC IS ALSO PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
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 CC
 DR EMBL; U04807; AAA18000.1; -
 DR EMBL; L23636; AAA39436.1; -
 DR EMBL; U29875; AAA90951.1; -
 DR EMBL; U29875; AAA90952.1; -
 DR EMBL; S76459; AAB33069.1; -
 DR EMBL; S76461; AAB33070.1; -
 DR EMBL; U44024; AAA93307.1; -
 DR EMBL; U44024; AAA93306.1; -
 DR MGD; MGI:95560; Flt3l.
 KW Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 232
 FT DOMAIN 27 189
 FT TRANSMEM 190 210
 FT TRANSMEM 211 232
 FT DOMAIN 211 232
 FT CARBOHYD 127 127
 FT CARBOHYD 152 152
 FT VARSPLIC 164 232
 FT VARSPLIC 164 169
 FT VARSPLIC 170 232
 FT CONFLICT 141 141
 FT CONFLICT 198 198
 SQ SEQUENCE 232 AA; 26141 MW; 3A3680D3CB69FBA6 CRC64;
 Query Match 61.8%; Score 768; DB 1; Length 232;
 Best Local Similarity 70.0%; Pred. No. 5.9e-58;
 Matches 163; Conservative 17; Mismatches 43; Indels 10; Gaps 4;

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QY 1 MTVLAPAWSP-TTYLLLLSSLSGTQDCSFQSPISDFAVKIRELSYLLQDYPVT 59
Db 1 MTVLAPAWSPSSLLLLLLSCLRCTPCDYFESHSPISSNFKVKFRELTDHLLKDPVT 60
QY 60 VASNLQDEELCGGLRWLVLAQRWMLKTVAGSKMQLLERNVTEIHFTVKCAFPFPPSC 119
Db 61 VAVNLQDEKHCALWSLFLAQRWIEQLTVAGSKMQLLLEDVNTIEHFTVCTFQPLPEC 120
QY 120 LRFVQTNISRLQETSEQLVALKPWITR--QNESRCLQLOCPDSSLPPLPWPSPRPLEAT 177
Db 121 LRFVQTNISHLKTDCTQLLALAPCIGKACQNFSCLEVQCQDPSSTLLPSPRSIALEAT 180
QY 178 APTAPOP---LLLLLLPVGLLLAAWCLHWQTRRRTPRGEQVPPVPS 227
Db 181 ELPEPRPQRLLLLLLLPITVLLAAWGLRQARRR---GELHPGVLP 229

RESULT 3
AT12_VZVD
ID AT12_VZVD STANDARD; PRT; 661 AA.
AC P09264;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DE 01-NOV-1990 (Rel. 16, Last annotation update)
DE ALPHA TRANS-INDUCING FACTOR 74 KDA PROTEIN.
GN 12.
OS Varicella-zoster virus (strain Dumas) (VZV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OC NCBI_TaxID=10338;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86306567; PubMed=3018124;
RA Davison A.J., Scott J.E.;
RT "The complete DNA sequence of varicella-zoster virus.";
RL J. Gen. Virol. 67:1759-1816(1986).
CC -1- FUNCTION: MODULATE ALPHA TRANS-INDUCING FACTOR-DEPENDENT
CC ACTIVATION OF ALPHA GENES
CC -----
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CC -----
DR EMBL; X04370; CAA27895.1; -
DR PIR; C27342; TNBE12.
KW Transcription regulation; Trans-acting factor.
SQ SEQUENCE 661 AA; 74272 MW; C5CA77A16D365379 CRC64;

Query Match 7.48; Score 92; DB 1; Length 661;
Best Local Similarity 26.68; Pred. No. 2.1;
Matches 61; Conservative 29; Mismatches 103; Indels 36; Gaps 11;

QY 19 LLSGLSGTDCS-----FOHSPISDFAVKI--RELSYLLQDYPVTVASNLQDEELCG- 71
Db 79 LTPSVLQSTHERSVLLGLHNNVPESLVSCMSNDVHGFQWQRYMETIQRCLDLKLSGD 138
QY 72 GLRWLVLAQRWMLKTVAGSKMQLLERNV-----TEIHFTVKCAFP-----PPSCLRFV 123
Db 139 GLW-WYVNTYVQWLKTVTGAQVPTVSEKVNKSKSTVLLFSSVVANKPIRHPFKSVI 197
QY 124 QTNISRLQETSEQLVALKPWITRQNSRCLQLOCPDSSLPPLPWPSP-RELEATAPAT 182
Db 198 NSDVRGICQELREALGAVQYK-----YFWR-----PDDTPNPSFDRIRVQIEAATAT 247
QY 183 QPPELLLLLPVGLLLAAWCLHWQTRRRTPRPGQVPPVPSQDILL 231
Db 248 GYGWMLWFLDWD-----ARVCRHLKQLQERRIRPRASV-----IPDDL 287
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RESULT 4
GBR2_HUMAN
ID GBR2_HUMAN STANDARD; PRT; 941 AA.
AC 075899; 075974; 075975; Q9UN9S; Q9UNR1; Q9PLR2;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2 PRECURSOR (GABA-B
DE RECEPTOR 2) (GABA-B-R2) (GB2) (GABABR2) (G PROTEIN-COUPLED RECEPTOR
DE 51) (GPR 51) (HC20).
GN GABR2 OR GPR51.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RX TISSUE=Cerebellum;
RX MEDLINE=99087321; PubMed=9872316;
RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,
RA Barnes A.A., Emson P., Foord S.M., Marshall F.H.;
RT "Heterodimerization is required for the formation of a functional
RT GABA(B) receptor.";
RL Nature 396:679-682(1998).
RN [2]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2A; 2B AND 2C).
RX TISSUE=Brain;
RX MEDLINE=20193514; PubMed=10727622;
RA Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";
RL Brain Res. 860:41-52(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RA Liu M., Parker R., McCreia K., Watson J., Baker E., Sutherland G.,
RA Herzog H.;
RT "Cloning and characterization of a novel human GABA-B receptor subtype
RT with high affinity for GABA and low affinity for baclofen.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RX TISSUE=Hippocampus;
RA Borowsky B., Laz T., Gerald C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RX TISSUE=Fetal brain;
RX MEDLINE=99189236; PubMed=10087195;
RA Ng G.Y.K., McDonald T., Bonner T., Rigby M., Heavens R., Whiting P.,
RA Chateaufneuf A., Coulombe N., Kargman S., Caskey T., Evans J.F.,
RA O'Neill G.P., Liu Q.;
RT "Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAB
RT receptors expressed predominantly in nervous tissues and mapped
RT proximal to the hereditary sensory neuropathy type 1 locus on
RT chromosome 9.";
RL Genomics 56:288-295(1999).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2A), AND VARIANTS PHE-628 AND ALA-869.
RX TISSUE=Brain;
RX MEDLINE=99263199; PubMed=10328880;
RA Martin S.C., Russek S.J., Farb D.H.;
RT "Molecular identification of the human GABABR2: cell surface
RT expression and coupling to adenylyl cyclase in the absence of
RT GABABR1.";
RL Mol. Cell. Neurosci. 13:180-191(1999).
RN [7]
RP R1A-R2 INTERACTION.
RX MEDLINE=99175124; PubMed=10075644;
RA Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R.,
RA Kargman S., Chateaufneuf A., Tsukamoto N., McDonald T., Whiting P.,
RA Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
RA Bonner T.I., O'Neill G.P.;
```


RT "Both hypertrophic and dilated cardiomyopathies are caused by mutation
RT of the same gene, delta-sarcoglycan, in hamster: an animal model of
RT disrupted dystrophin-associated glycoprotein complex.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:13873-13878(1997).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN-FIB: TISSUE-Skeletal muscle;
RX MEDLINE=95278335; PubMed=7758576;
RA Roberts S.L., Campbell K.P.;
RT "Adhalin mRNA and cDNA sequence are normal in the cardiomyopathic
RT hamster.";
RL FEBS Lett. 364:245-249(1995).

CC -1- FUNCTION: COMPONENT OF THE SARCOGLYCAN COMPLEX, A SUBCOMPLEX OF
CC THE DYSTROPHIN-GLYCOPROTEIN COMPLEX WHICH FORMS A LINK BETWEEN THE
CC F-ACTIN CYTOSKELETON AND THE EXTRACELLULAR MATRIX.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SARCOLEMMA
CC (POTENTIAL).
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SKELETAL AND
CC HEART MUSCLE.
CC -1- SIMILARITY: BELONGS TO THE SARCOGLYCAN ALPHA/EPSILON FAMILY.

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CC -----
DR EMBL: D83651; BAA12025.1; -
DR EMBL: U21677; AAA81645.1; -
KW Cytoskeleton; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 387 ALPHA-SARCOGLYCAN.
FT DOMAIN 24 290 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 291 311 POTENTIAL.
FT DOMAIN 312 387 POTENTIAL.
FT DOMAIN 209 335 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 387 AA; 43326 MW; D8599C0FAF646C3F CRC64;

Query Match 7.28; Score 89; DB 1; Length 387;
Best Local Similarity 23.48; Pred. No. 2;
Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps 14;

```
QY 11 TTYLLLLSSGLSGTDCSFOHSPISDDFAVKIRELSYLLQDPYVTVASNLQDEELC 70
Db 115 TTRQLLLLI-----EDPEGRPLPYQAEFLVRSHDVEYL-----PSTPANREL--TAL 161

QY 71 GGLWRL-----VLAQRWMLKTVAGSKMQLLRVNTIHFVT-----K 110
Db 162 GGLWELGELQLNLTSLDRGRVPLTEGRKEGYIKVGSATPFSTCKMVASPDSVAR 221

QY 111 CAQOPPP--SC-----LRFVNINRLLQETSEQLVALKPWITRQNSRCLQLQCPD 161
Db 222 CAQOPPLLCYSLAPHFVDMCNVSLDKSVPELD-----EVPTPGD 266

QY 162 SSTLPWPSPRPLEAT-----APTAPQPLLLLLLVGLLLLAANC----- 204
Db 267 GILEHDFPFCPTAQRGDFLADALVTLVPLLVALLL---TLLAVIMCRRREGQLKRD 323

QY 205 -----LHWQTRRRTRPR-----GEQVPP--VPSPQ--DLL 231
Db 324 MATSDIQMVHCHTGHNGTEELRQMAARVPRPLSTLPMFNVRTGERLPPRVDSQAQVPLI 383

QY 232 LVEH 235
Db 384 LDQH 387
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RESULT 6

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S3A1_HUMAN
ID S3A1_HUMAN STANDARD; PRT; 793 AA.
AC Q15459;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE SPLICING FACTOR 3 SUBUNIT 1 (SPLICOSOME ASSOCIATED PROTEIN 114) (SAP
DE 114) (SF3A120).
GN SF3A1 OR SAP114.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079958; PubMed=7489498;
RA Kraemer A., Mulhauser F., Wersig C., Groning K., Bilbe G.;
RT "Mammalian splicing factor SF3a120 represents a new member of the
RT SURP family of proteins and is homologous to the essential splicing
RT factor PRP21p of Saccharomyces cerevisiae.";
RL RNA 1:260-272(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX Kraemer A., Blandford M.;
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP CHARACTERIZATION OF THE SPLICOSOME.
RX PubMed=10882114;
RA Das R., Zhou Z., Reed R.;
RT "Functional association of U2 snRNP with the ATP-independent
RT spliceosomal complex E.";
RL Mol. Cell 5:779-787(2000).
CC -1- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A'
CC COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE
CC BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT
CC BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS
CC ESSENTIAL. IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE
CC INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.
CC -1- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3A WHICH IS COMPOSED OF
CC THREE SUBUNITS; SF3A3/SAP61, SF3A2/SAP62, SF3A1/SAP114. SF3A
CC ASSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TO
CC FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP).
CC INTERACTS WITH SF3A3.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.
CC -1- SIMILARITY: CONTAINS 1 UBQUITIN-LIKE DOMAIN.
CC -1- SIMILARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRP21.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X85237; CAA59494.1; -
DR EMBL: AC004997; AAC23435.1; -
DR MIN; 605595; -
DR InterPro; IPR000061; Surp.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF01805; Surp. 2.
DR Pfam; PF00240; ubiquitin; 1.
DR SMART; SM00213; UBO; 1.
DR PROSITE; PS00553; UBQUITIN_2; 1.
DR SPLICOSOME; mRNA processing; mRNA splicing; Nuclear protein; Repeat.
KW REPEAT 52 94 SURP MOTIF 1.
KW REPEAT 166 208 SURP MOTIF 2.
KW DOMAIN 707 793 UBQUITIN-LIKE.
KW DOMAIN 10 16 POLY-PRO.
KW DOMAIN 118 122 POLY-GLN.
KW DOMAIN 260 267 POLY-GLU.
KW DOMAIN 369 372 POLY-PRO.
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FT DOMAIN 557 560 POLY-PRO.
FT DOMAIN 672 675 POLY-PRO.
SQ SEQUENCE 793 AA; 8886 MW; 7259F1EC4577305C CRC64;

Query Match 7.2%; Score 89; DB 1; Length 793;
Best Local Similarity 22.3%; Pred. No. 4.6;
Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

QY 4 LAPASPTTYVLLLLLSGLSTQDCSQHSPISSDFAVKIRELSYLLLODPVTVASN 63
DB 401 LPPAPADPDLV-----SPITGE---KI-----PASK 424

QY 64 LQDEELCGGLRWLVLAQRWME-RLKTV-----AGSKMOGLLERNVTEIHF 107
DB 425 MOEHRIG-----LLDPRLQEDRSIREKQSDDEYVAPGLDIESLKQLAER-RDIFG 478

QY 108 VTKCA-----FQPPPSCLRF-----VOTNISRLQETSEQLVALKPMI 145
DB 479 VEETAIGKIGBEEIQPEKVTWDHSGSMARTQQAQANIT--LQEQLEAIHKAGLV 536

QY 146 ----TRQNF--SRCLELOCP-----DSTLP-----PPWSPRLEAT----APT 180
DB 537 PEDTKEKIGSKPNIPPOPPPSATIPSPAPITSVPRPPTMPPPVRTTWSAVPV 596

QY 181 APQPLLPLLLLVGLLLAAWCLHWQTR-----RRTPRGQVPP---VPSP 227
DB 597 MRPPMASVVRLLPGSVIAPMPPIIHAPINVPMPSPAPPINAPRPPMIVPTAFVAP 656

RESULT 7
ID TNRC_MOUSE STANDARD; PRT; 415 AA.
AC P50284.
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
GN LTBR OR TNFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CVB; TISSUE=Lung;
RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression."
RL J. Immunol. 155:5280-5288(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8596432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT sequence trap and chromosomal mapping."
RL Genomics 30:312-319(1995).
RC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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DR EMBL: U29173; AAG8964.1; -
DR EMBL: L38423; AAB00846.1; -
DR EMBL: U30798; AAB81334.1; -
DR HSSP: P25942; ICDF.
DR MGD: MGI:104875; Ltbr.
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF00020; TNFR_C6; 3.
DR ProDom: PD000771; TNFR_C6; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00050; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 415
FT DOMAIN 31 223
FT TRANSMEM 224 244
FT DOMAIN 245 415
FT DOMAIN 42 213
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 170
FT REPEAT 171 213
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 150
FT DISULFID 142 169
FT DISULFID 172 187
FT CARBOHYD 40 40
FT CARBOHYD 179 179
SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;

Query Match 7.0%; Score 87.5; DB 1; Length 415;
Best Local Similarity 24.4%; Pred. No. 2.9;
Matches 39; Conservative 20; Mismatches 52; Indels 49; Gaps 8;

QY 110 KCAFPQPPSCL-----RFV-----QTNISRLQETSEQLVALKPWTRQNF 151
DB 123 ECRQCPGMSCVLDNECVHCEERLVLCQPTAEVDEIMDVCVPCPKPGHQTSS 182

QY 152 RCLELOCPDSSLTLPWPSPRPLEATP-----TAPQPLLPLLLLVGLL--- 198
DB 183 P--RARCQPHTRC-----EIQGLVEAAPGTSYSDTICKNPPEPGAMLLALLSLVFL 235

QY 199 ----LAAAWCLHWQTR-----RRTPRGQVPPVPSQ 228
DB 236 FTVVLACAMRHPSLCKRLKLTLLKRHPE-GEESPPCAPR 274

RESULT 8
MP1P_DROME
ID MP1P_DROME STANDARD; PRT; 479 AA.
AC F20483; Q9VAL9;
DT 01-FEB-1991 (Rel. 17, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE M-PHASE INDUCER PHOSPHATASE (EC 3.1.3.48) (STRING PROTEIN) (CDC25-LIKE
DE PROTEIN).
GN STG OR CDC25 OR CG1395.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89195217; PubMed=2702688;
RA Edgar B.A., O'Farrell P.H.;
```


CC -|- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
 CC -|- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
 CC
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 CC

DR EMBL: L26525; AAA21089.1; -
 DR HSP; P11362; IFGI.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000421; FA58.C.
 DR InterPro: IPR002011; Raptor_tyr_kin_II.
 DR InterPro: IPR001245; Tyr_kin.
 DR Pfam: PF00754; F5_F8_type_C; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00231; FA58C; 1.
 DR SMART: SM00219; TyKc; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR PROSITE: PS01285; FA58C.1; 1.
 DR PROSITE: PS01286; FA58C.2; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR Transferrase: Tyrosine-protein kinase; Glycoprotein; Signal;
 KW Phosphorylation; Transmembrane; Receptor; ATP-binding.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 910 EPITHELIAL DISCOIDIN DOMAIN RECEPTOR 1.
 FT DOMAIN 20 413 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 414 440 POTENTIAL.
 FT DOMAIN 441 910 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 32 186 F5/8 TYPE C (PHOSPHOLIPID-BINDING, POTENTIAL).
 FT DOMAIN 378 412 GLY/PRO-RICH.
 FT DOMAIN 473 598 GLY/PRO-RICH.
 FT DOMAIN 607 902 PROTEIN KINASE.
 FT NP_BIND 613 621 ATP (BY SIMILARITY).
 FT BINDING 652 652 ATP (BY SIMILARITY).
 FT ACT_SITE 763 763 BY SIMILARITY.
 FT DISULFID 32 186 BY SIMILARITY.
 FT MOD_RES 510 510 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 789 789 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 793 793 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 794 794 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 910 AA; 101164 MW; 7E7F9A1DCB029806 CRC64;

Query Match 7.0%; Score 87; DB 1; Length 910;
 Best Local Similarity 24.5%; Pred. No. 8;
 Matches 38; Conservative 12; Mismatches 35; Indels 70; Gaps 9;
 QY 143 PWTRQNSRLELOCPDSSLTLP--PW---SPRLENTA---PTAPQP----- 184
 Db 356 PWLSEIFSIDV-VNDSSTDPFPPAPWPPGPPPTNFSLEPRGQOPVAKESPTA 414
 QY 185: -----PLLLLLLVGLLLLAAACLHWQR-----TRRR-----T 214
 Db 415 ILIGCLVAIILLALLIALML-----NRLHWRLLSKAERRVLEELTVHLSVPGDTILIN 470
 QY 215 PRGEQVPP-----VPSQDILL 232
 Db 471 NRPGRPPPPYQPRGRGTPTHSAPCVNGSALLL 505

RESULT 10
 DDR1_MOUSE

ID DDR1_MOUSE STANDARD; PRT; 911 AA.
 AC Q03146;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE EPITHELIAL DISCOIDIN DOMAIN RECEPTOR 1 PRECURSOR (EC 2.7.1.112)
 DE (TYROSINE-PROTEIN KINASE CAK) (CELL ADHESION KINASE) (TYROSINE KINASE
 DE DR) (DISCOIDIN RECEPTOR TYROSINE KINASE) (PROTEIN-TYROSINE KINASE
 DE MPK-6).
 GN DDR1 OR EDDR1 OR CAK OR MPK6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=C57BL;
 RX MEDLINE=96204002; PubMed=8622863;
 RA Perez J.L., Jing S.Q., Wong T.W.;
 RT "Identification of two isoforms of the Cak receptor kinase that are
 RT coexpressed in breast tumor cell lines.";
 RL Oncogene 12:1469-1477(1996).
 RN [2]
 RP SEQUENCE OF 766-822 FROM N.A.
 RC STRAIN=C57BL; TISSUE=Embryonic brain;
 RX MEDLINE=93096484; PubMed=1281307;
 RA Gillardi-Hebenstreit P., Nieto M.A., Frain M., Mattei M.-G.,
 RA Chesler A., Wilkinson D.G., Charney P.;
 RT "An Eph-related receptor protein tyrosine kinase gene segmentally
 RT expressed in the developing mouse hindbrain.";
 RL Oncogene 7:2499-2506(1992).
 CC -|- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND
 CC RECOGNITION (BY SIMILARITY).
 CC -|- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -|- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -|- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CAK I (SHOWN HERE) AND CAK II;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER BY THE
 CC ABSENCE OF A 37 RESIDUES SEGMENT.
 CC -|- TISSUE SPECIFICITY: THE PREDOMINANT ISOFORM CAK I, IS EXPRESSED IN
 CC DEVELOPING EMBRYO AND ADULT BRAIN; CAK II IS EXPRESSED IN VARIOUS
 CC EPITHELIAL CELLS.
 CC -|- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF TYR-PROTEIN
 CC KINASES.
 CC -|- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
 CC -|- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES.
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 CC
 CC EMBL: L57509; AAB05209.1; -
 CC EMBL: X57240; CAA040516.1; -
 CC PIR: S30502; S30502.
 CC HSP; P11362; IFGI.
 CC MGD; MGI:99216; Ddr1.
 CC InterPro: IPR000719; Euk_pkinase.
 CC InterPro: IPR000421; FA58.C.
 CC InterPro: IPR002011; Raptor_tyr_kin_II.
 CC InterPro: IPR001245; Tyr_kin.
 CC Pfam: PF00754; F5_F8_type_C; 1.
 CC Pfam: PF00069; pkinase; 1.
 CC SMART: SM00231; FA58C; 1.
 CC SMART: SM00219; TyKc; 1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 CC PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 CC PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 CC PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.

FT CONFICT 161 LLA -> RHE (IN REF. 3).
 SQ SEQUENCE 282 AA; 30674 MW; DDB2F907CA0215A0 CRC64;

Query Match 6.8%; Score 85; DB 1; Length 282;
 Best Local Similarity 29.9%; Pred. No. 3;
 Matches 38; Conservative 7; Mismatches 38; Indels 44; Gaps 6;

QY 144 WIT-RNFSRCLQCOQPSSTLPPWSPRP--LEATA-----178
 Db 66 WMTVERDFTALLPPLPPGTLPQP-SPTPPDLEAMSLKKELEQMEDFFLDAPLPP 124
 QY 179 ---PTAPQPLLILLPLVL-----LLAAAWCLH--WQTRRTTRPGEQ 220
 Db 125 PSPPLPPPPAPSLPSLPSLPPQPPVLDLTLAIYCRNEAQEEVGMPLPPQ 184
 QY 221 VPPVSP 227
 Db 185 QPPVSP 191

RESULT 14
 FCGN_RAT STANDARD; PRT; 366 AA.
 AC P13599;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE IGG RECEPTOR FCN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC
 DE RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN).
 GN FCGRT OR FCRN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID:10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=WISTAR;
 RX MEDLINE=89097257; PubMed=2911353;
 RA Smolter N.E., Mostov K.E.;
 RL "An Fc receptor structurally related to MHC class I antigens.";
 RN Nature 337:184-187(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Epithelium;
 RX MEDLINE=90315866; PubMed=2534798;
 RA Smolter N.E., Mostov K.E.;
 RL "Cloning and expression of the neonatal rat intestinal Fc receptor, a
 RL major histocompatibility complex class I antigen homolog.";
 RN Cold Spring Harb. Symp. Quant. Biol. 54:571-580(1989).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=9059482; PubMed=7969498;
 RA Burmeister W.P., Huber A.H., Bjorkman P.J.;
 RL "Crystal structure of the complex of rat neonatal Fc receptor with
 RL Fc.";
 RN Nature 372:379-383(1994).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=98154319; PubMed=9493268;
 RA Vaughn D.E., Bjorkman P.J.;
 RL "Structural basis of pH-dependent antibody binding by the neonatal Fc
 RL receptor.";
 RN Structure 6:63-73(1998).
 CC -1- FUNCTION: BINDS TO THE FC REGION OF MONOMERIC IMMUNOGLOBULINS
 CC GAMMA. MEDIATES THE SELECTIVE UPTAKE OF IGG FROM MILK AND HELPS
 CC NEWBORN ANIMALS TO ACQUIRE PASSIVE IMMUNITY. IGG IN THE MILK IS
 CC BOUND AT THE APICAL SURFACE OF THE INTESTINAL EPITHELIUM. THE
 CC RESULTANT FCN-IGG COMPLEXES ARE TRANSCYTOSED ACROSS THE
 CC INTESTINAL EPITHELIUM AND IGG IS RELEASED FROM FCN INTO BLOOD OR
 CC TISSUE FLUIDS (BY SIMILARITY).
 CC -1- SUBUNIT: FCN COMPLEX CONSIST OF TWO SUBUNITS: P51, AND P14 WHICH
 CC IS EQUIVALENT TO BETA-2-MICROGLOBULIN. IT FORMS AN MCH CLASS I-

CC LIKE HETERODIMER.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: INTESTINAL EPITHELIUM.
 CC -1- SIMILARITY: STRONG, TO MHC CLASS I ANTIGENS.
 CC
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 CC
 CC EMBL; X14323; CA32503.1; -;
 CC EMBL; M35495; AAA4611.1; -;
 CC PIR; S02117; S02117;
 CC PIR; A37374; A37374;
 CC PDB; 1FRT; 14-FEB-95.
 CC PDB; 3FRU; 10-JUN-98.
 CC InterPro; IPR003006; Ig_MHC.
 CC InterPro; IPR003597; Ig_C1.
 CC InterPro; IPR001220; Lectin_legb.
 CC InterPro; IPR001039; MHC_I.
 CC Pfam; PF00047; Ig; 1.
 CC Pfam; PF00129; MHC_I; 1.
 CC ProDom; PD000050; MHC_I; 1.
 CC SMART; SM00407; IGC1; 1.
 CC PROSITE; PS00290; IG_MHC; 1.
 CC Igg-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; 3D-structure.
 FT SIGNAL 1 22
 FT CHAIN 23 366 IGG RECEPTOR FCN LARGE SUBUNIT P51.
 FT DOMAIN 23 111 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 112 201 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 202 291 EXTRACELLULAR ALPHA-3.
 FT DOMAIN 292 298 CONNECTING PEPTIDE.
 FT TRANSMEM 299 322 POTENTIAL.
 FT DOMAIN 323 366 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 120 183 BY SIMILARITY.
 FT DISULFID 222 276 BY SIMILARITY.
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 366 AA; 40168 MW; 8ABBF2873A698BB5 CRC64;

Query Match 6.8%; Score 85; DB 1; Length 366;
 Best Local Similarity 22.2%; Pred. No. 4.1;
 Matches 51; Conservative 21; Mismatches 66; Indels 92; Gaps 11;

QY 46 RELSDYLDQYPVTVASNLQDEELCGGLWRLVLAQRNME----RLKTVAGSKMOGLLERV 101
 Db 173 RKESEFLTSCP-----ERLLGHLGRQNLKWKPEPSMLKARPNGSSVL---220
 QY 102 NTEIHFTVCA---FQPPPSCLRFVQTNISRLLOETSEQLVALKPWITRONFSRC-----153
 Db 221 -----TCAAFSFPPELKFRLRGLA-----SGSGNCSTGPN 253
 QY 154 -----LEL-----QCQPDSSLTLPWPSPRPLEATAPQPPPLLLLLLLPVG 195
 Db 254 GGSFHWASLLEVKRDEHHYQCVHEGLAQPLT---VLDSPARSPVPVWGI--G 307
 QY 196 LLLLA---AAWCLHWQTRRTTRP-----PGEQVPPVPSQ 228
 Db 308 LLLVVAAGVLLWNRMSGLPAPWLSLSDGDDSGDLLPGNLPPEAPQ 357
 RESULT 15
 MNT_HUMAN STANDARD; PRT; 582 AA.
 ID MNT_HUMAN
 AC Q99583
 DT 15-DEC-1998 (Rel. 37, Created)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 1, 2002, 06:13:54 ; Search time 64.79 seconds
(without alignments)
81.622 Million cell updates/sec

Title: US-08-162-407-6

Perfect score: 1242

Sequence: 1 MVLAPAWSPTYLLLLLLL.....RPGQVPPVPQDLLLVEH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA.*

1: /cgn2.6/ptodata/2/iaa/5A_COMB.pep.*

2: /cgn2.6/ptodata/2/iaa/5B_COMB.pep.*

3: /cgn2.6/ptodata/2/iaa/6A_COMB.pep.*

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5: /cgn2.6/ptodata/2/iaa/PCTUS_COMB.pep.*

6: /cgn2.6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1242	100.0	235	1	US-08-243-545-6
2	1242	100.0	235	2	US-08-993-962-6
3	1242	100.0	235	4	US-09-160-841-6
4	1242	100.0	235	4	US-09-109-100-1
5	1242	100.0	235	5	PCT-US94-05365-6
6	1124	90.5	212	4	US-09-109-100-10
7	1114	89.7	209	4	US-09-109-100-18
8	1110	88.4	209	4	US-09-109-100-9
9	1110	88.4	209	4	US-09-109-100-12
10	1110	88.4	209	4	US-09-109-100-14
11	1110	88.4	209	4	US-09-109-100-17
12	1108	88.2	209	4	US-09-109-100-11
13	1108	88.2	209	4	US-09-109-100-15
14	1107	88.1	209	4	US-09-109-100-13
15	1106	88.0	209	4	US-09-109-100-8
16	1100	88.6	209	4	US-09-109-100-16
17	768.5	61.9	231	1	US-08-243-545-2
18	768.5	61.9	231	2	US-08-993-962-2
19	768.5	61.9	231	4	US-09-160-841-2
20	768.5	61.9	231	5	PCT-US94-05365-2
21	765.5	61.6	231	1	US-08-220-379B-7
22	765.5	61.6	231	5	PCT-US95-03866-6
23	505.5	40.8	137	4	US-09-109-100-19
24	154	12.4	42	5	PCT-US94-05150-17
25	91.5	7.4	675	1	US-08-317-522A-9
26	91.5	7.4	675	1	US-08-439-818A-9
27	91.5	7.4	675	2	US-08-751-965-9

28 91.5 7.4 675 2 US-08-738-975-9 Sequence 9, Appl
29 91.5 7.4 675 2 US-08-728-626-9 Sequence 9, Appl
30 91.5 7.4 675 2 US-08-808-599A-9 Sequence 9, Appl
31 87.5 7.0 415 4 US-09-006-353A-6 Sequence 6, Appl
32 85 6.8 366 1 US-08-004-493-8 Sequence 8, Appl
33 84.5 6.8 913 1 US-08-445-640-4 Sequence 4, Appl
34 84.5 6.8 913 3 US-08-170-558-4 Sequence 4, Appl
35 84.5 6.8 913 3 US-08-447-314-4 Sequence 4, Appl
36 84.5 6.8 913 3 US-08-445-461-4 Sequence 4, Appl
37 84 6.8 107 4 US-09-220-528-52 Sequence 52, Appl
38 84 6.8 220 4 US-09-220-528-26 Sequence 26, Appl
39 83.5 6.7 429 1 US-07-964-580-2 Sequence 2, Appl
40 83.5 6.7 429 5 PCT-US93-02024-2 Sequence 2, Appl
41 83.5 6.7 671 3 US-09-121-321-16 Sequence 16, Appl
42 83.5 6.7 671 4 US-08-933-803A-16 Sequence 16, Appl
43 83 6.7 28 5 PCT-US94-05150-12 Sequence 12, Appl
44 83 6.7 758 1 US-07-756-250-16 Sequence 16, Appl
45 82.5 6.6 249 2 US-08-632-514C-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-243-545-6
; Sequence 6, Application US/08243545
; Patent No. 5554512
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,545
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids

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;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-243-545-6

Query Match      100.0%; Score 1242; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e-117; Indels 0; Gaps 0;
Matches 235; Conservative 0; Mismatches 0;

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Db 1 MTVLAPAWSPTTYLLLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
QY 61 ASNLQDEELCGGLRWLRVLAQRWMLKTVAGSKMOGLLERVNTIHFVTKCAFQPPPSCL 120
Db 61 ASNLQDEELCGGLRWLRVLAQRWMLKTVAGSKMOGLLERVNTIHFVTKCAFQPPPSCL 120
QY 121 RFVOTNISRLQETSEQLVAKPWITRONFSCLELQCCPDSSTLPPWSPRPLEATAPT 180
Db 121 RFVOTNISRLQETSEQLVAKPWITRONFSCLELQCCPDSSTLPPWSPRPLEATAPT 180
QY 181 APQPPLLLLLPVGLLLAAACWCLHWQTRRRTPRPGEQVPPVPSQDLLLLVEH 235
Db 181 APQPPLLLLLPVGLLLAAACWCLHWQTRRRTPRPGEQVPPVPSQDLLLLVEH 235

RESULT 2
US-08-993-962-6
; Sequence 6, Application US/08993962
; Patent No. 5843423
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,962
; FILING DATE: December 18, 1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644

;
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-993-962-6

Query Match      100.0%; Score 1242; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e-117; Indels 0; Gaps 0;
Matches 235; Conservative 0; Mismatches 0;

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Db 1 MTVLAPAWSPTTYLLLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
QY 61 ASNLQDEELCGGLRWLRVLAQRWMLKTVAGSKMOGLLERVNTIHFVTKCAFQPPPSCL 120
Db 61 ASNLQDEELCGGLRWLRVLAQRWMLKTVAGSKMOGLLERVNTIHFVTKCAFQPPPSCL 120
QY 121 RFVOTNISRLQETSEQLVAKPWITRONFSCLELQCCPDSSTLPPWSPRPLEATAPT 180
Db 121 RFVOTNISRLQETSEQLVAKPWITRONFSCLELQCCPDSSTLPPWSPRPLEATAPT 180
QY 181 APQPPLLLLLPVGLLLAAACWCLHWQTRRRTPRPGEQVPPVPSQDLLLLVEH 235
Db 181 APQPPLLLLLPVGLLLAAACWCLHWQTRRRTPRPGEQVPPVPSQDLLLLVEH 235

RESULT 3
US-09-160-841-6
; Sequence 6, Application US/09160841
; Patent No. 6190655
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,841
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 587-0430
```

TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-160-841-6

Query Match 100.0%; Score 1242; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
DB 1 MTVLAPAWSPTTYLLLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
QY 61 ASNLQDEELCGGLRLVLAQRWMLKTVAGSKMGLLRVNTIHFVTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLRLVLAQRWMLKTVAGSKMGLLRVNTIHFVTKCAFQPPPSCL 120
QY 121 RVQTNISRLQETSEQLVAKPWITRONFSCLELQCPDSTLPPWSPRPLEATPT 180
DB 121 RVQTNISRLQETSEQLVAKPWITRONFSCLELQCPDSTLPPWSPRPLEATPT 180
QY 181 APQPLLLLLLPVGLLLAAACWLHWQTRRTTRPRGQVPPVPSQDILLVEH 235
DB 181 APQPLLLLLLPVGLLLAAACWLHWQTRRTTRPRGQVPPVPSQDILLVEH 235

RESULT 4

US-09-109-100-1
Sequence 1, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-1

Query Match 100.0%; Score 1242; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MTVLAPAWSPTTYLLLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
QY 61 ASNLQDEELCGGLRLVLAQRWMLKTVAGSKMGLLRVNTIHFVTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLRLVLAQRWMLKTVAGSKMGLLRVNTIHFVTKCAFQPPPSCL 120
QY 121 RVQTNISRLQETSEQLVAKPWITRONFSCLELQCPDSTLPPWSPRPLEATPT 180
DB 121 RVQTNISRLQETSEQLVAKPWITRONFSCLELQCPDSTLPPWSPRPLEATPT 180
QY 181 APQPLLLLLLPVGLLLAAACWLHWQTRRTTRPRGQVPPVPSQDILLVEH 235
DB 181 APQPLLLLLLPVGLLLAAACWLHWQTRRTTRPRGQVPPVPSQDILLVEH 235

RESULT 5

PCT-US94-05365-6
Sequence 6, Application PC/TUS9405365
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05365
FILING DATE: May 24, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: -to be assigned-
FILING DATE: May 11, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,502
FILING DATE: March 7, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,407
FILING DATE: December 3, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-05365-6

Query Match 100.0%; Score 1242; DB 5; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPTTYLLLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60
DB 1 MTVLAPAWSPTTYLLLSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPVT 60

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Db	61	ASNLDDELGGGLRWRLVLAQRWNERLUKTVAGSKMQGILLERNVTEIHFTVKCAFQPPSPCL	120
QY	121	RFVQTNISRLLOETSEQLVALKPWITRQNFSCRLEQCQPDSTLPPWSPRPLEATAPT	180
Db	121	RFVQTNISRLLOETSEQLVALKPWITRQNFSCRLEQCQPDSTLPPWSPRPLEATAPT	180
QY	181	APQPPDLLLLLLPVGLLLLLAAACLHWQTRRRTPRPGEQVPPVPSQDLLLVEH	235
Db	181	APQPPDLLLLLLPVGLLLLLAAACLHWQTRRRTPRPGEQVPPVPSQDLLLVEH	235

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RESULT      6
US-09-109-100-10
; Sequence 10, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ.ID NOS.: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-10

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Query Match	90.5%;	Score 1124;	DB 4;	Length 212;
Best Local Similarity	100.0%;	Prod. No. 9.5e-106;		
Matches 211;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	25	SGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDELCGGLRWLVLAQRWME	84	
Db	2	SGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDELCGGLRWLVLAQRWME	61	
QY	85	RLKTVAGSKMOGLLERVNTIEHFVTKCAFOPPPSCLRFVQTNISRLIQETSEQLVALKPW	144	
Db	62	RLKTVAGSKMOGLLERVNTIEHFVTKCAFOPPPSCLRFVQTNISRLIQETSEQLVALKPW	121	
QY	145	ITRQNSRCLLELOCQPDSSITLPPWPSPRPLEATAPTAPQPPLLLLLLLPGVGLLLLAAMC	204	
Db	122	ITRQNSRCLLELOCQPDSSITLPPWPSPRPLEATAPTAPQPPLLLLLLLPGVGLLLLAAMC	181	
QY	205	LHWQTRRRTRPRGEQVPPVPSPODLLLVEH	235	
Db	182	LHWQTRRRTRPRGEQVPPVPSPODLLLVEH	212	A4

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RESULT      7
US-09-109-100-18
; Sequence 18, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT-3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 18
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-18

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[illegible]

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RESULT      8
US-09-109-100-9
; Sequence 9, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT-3 L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-9

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Query Match	89.4%	Score 1110;	DB 4;	Length 209;
Best Local Similarity	99.5%;	Pred. No. 2.4e-104;		
Matches 208;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps 0;				
QY	27	TODCSFOHSPISDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL	86	
Db	1	TODCSFOHSPISDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL	60	
QY	87	KTVAGSKMOGLLERVNTIHFVTKAFQPPSPSCLRFVQTNISRLQETSEOLVALKPWIT	146	
Db	61	KTVGSKMOGLLERVNTIHFVTKAFQPPSPSCLRFVQTNISRLQETSEOLVALKPWIT	120	
QY	147	RQNFSCRLELQCQDSTLPPWPSPRPLEATAPAPQPPLLLLLLLLPVGLLLLAAAAWCLH	206	
Db	121	RQNFSCRLELQCQDSTLPPWPSPRPLEATAPAPQPPLLLLLLLLPVGLLLLAAAAWCLH	180	
QY	207	WQTRRTTRPGEQVPVPSPQDLLLLVEH	235	
Db	181	WQTRRTTRPGEQVPVPSPQDLLLLVEH	209	

RESULT 9
US-09-109-100-12
; Sequence 12, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C

;; CURRENT FILING DATE: 1998-07-02
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 12
;; LENGTH: 209
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-109-100-12

Query Match 89.4%; Score 1110; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 2.4e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLRWLVLAQRWML 86
Db 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLRWLVLAQRWML 60
QY 87 KTVAGSKMOGLLERVNTTEHFVTKAFQPPSCSLRFVQTNISRLQETSEQLVALKPWIT 146
Db 61 KTVAGSKMOGLLERVNTTEHFVTKAFQPPSCSLRFVQTNISRLQETSEQLVALKPWIT 120
QY 147 RNFSCLELQCPDSTLPPWSPRPLEATAPTAQPPLLLLLLPVGLLLAAWCLH 206
Db 121 RNFSCLELQCPDSTLPPWSPRPLEATAPTAQPPLLLLLLPVGLLLAAWCLH 180
QY 207 WQTRRTTRPGEQVPPVSPQDLLLLVEH 235
Db 181 WQTRRTTRPGEQVPPVSPQDLLLLVEH 209

RESULT 10

US-09-109-100-14
;; Sequence 14, Application US/09109100C
;; Patent No. 6291661
;; GENERAL INFORMATION:
;; APPLICANT: Graddis, Thomas J.
;; APPLICANT: McGrew, Jeffrey T.
;; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
;; FILE REFERENCE: 03260.0028
;; CURRENT APPLICATION NUMBER: US/09/109,100C
;; CURRENT FILING DATE: 1998-07-02
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 14
;; LENGTH: 209
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-109-100-14

Query Match 89.4%; Score 1110; DB 4; Length 209; *
Best Local Similarity 99.5%; Pred. No. 2.4e-104;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLRWLVLAQRWML 86
Db 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLRWLVLAQRWML 60
QY 87 KTVAGSKMOGLLERVNTTEHFVTKAFQPPSCSLRFVQTNISRLQETSEQLVALKPWIT 146
Db 61 KTVAGSKMOGLLERVNTTEHFVTKAFQPPSCSLRFVQTNISRLQETSEQLVALKPWIT 120
QY 147 RNFSCLELQCPDSTLPPWSPRPLEATAPTAQPPLLLLLLPVGLLLAAWCLH 206
Db 121 RNFSCLELQCPDSTLPPWSPRPLEATAPTAQPPLLLLLLPVGLLLAAWCLH 180
QY 207 WQTRRTTRPGEQVPPVSPQDLLLLVEH 235
Db 181 WQTRRTTRPGEQVPPVSPQDLLLLVEH 209

RESULT 11

US-09-109-100-17
;; Sequence 17, Application US/09109100C
;; Patent No. 6291661
;; GENERAL INFORMATION:
;; APPLICANT: Graddis, Thomas J.
;; APPLICANT: McGrew, Jeffrey T.
;; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
;; FILE REFERENCE: 03260.0028
;; CURRENT APPLICATION NUMBER: US/09/109,100C
;; CURRENT FILING DATE: 1998-07-02
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 17
;; LENGTH: 209
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-109-100-17

Query Match 89.4%; Score 1110; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 2.4e-104;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLRWLVLAQRWML 86
Db 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLRWLVLAQRWML 60
QY 87 KTVAGSKMOGLLERVNTTEHFVTKAFQPPSCSLRFVQTNISRLQETSEQLVALKPWIT 146
Db 61 KTVAGSKMOGLLERVNTTEHFVTKAFQPPSCSLRFVQTNISRLQETSEQLVALKPWIT 120
QY 147 RNFSCLELQCPDSTLPPWSPRPLEATAPTAQPPLLLLLLPVGLLLAAWCLH 206
Db 121 RNFSCLELQCPDSTLPPWSPRPLEATAPTAQPPLLLLLLPVGLLLAAWCLH 180
QY 207 WQTRRTTRPGEQVPPVSPQDLLLLVEH 235
Db 181 WQTRRTTRPGEQVPPVSPQDLLLLVEH 209

RESULT 12

US-09-109-100-11
;; Sequence 11, Application US/09109100C
;; Patent No. 6291661
;; GENERAL INFORMATION:
;; APPLICANT: Graddis, Thomas J.
;; APPLICANT: McGrew, Jeffrey T.
;; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
;; FILE REFERENCE: 03260.0028
;; CURRENT APPLICATION NUMBER: US/09/109,100C
;; CURRENT FILING DATE: 1998-07-02
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 11
;; LENGTH: 209
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-109-100-11

Query Match 89.2%; Score 1108; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 3.8e-104;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLRWLVLAQRWML 86
Db 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPTVASNLQDEELCGGLRWLVLAQRWML 60
QY 87 KTVAGSKMOGLLERVNTTEHFVTKAFQPPSCSLRFVQTNISRLQETSEQLVALKPWIT 146
Db 61 KTVAGSKMOGLLERVNTTEHFVTKAFQPPSCSLRFVQTNISRLQETSEQLVALKPWIT 120
QY 147 RNFSCLELQCPDSTLPPWSPRPLEATAPTAQPPLLLLLLPVGLLLAAWCLH 206

Db 121 RQNFSCLELQCPDSTLPPWSPRLEATAPOPPPLLLLLLPGVGLLLAAACWLH 180
QY 207 WQTRRRTPRGEQVPPVSPQDLLLLVEH 235
Db 181 WQTRRRTPRGEQVPPVSPQDLLLLVEH 209

RESULT 13
US-09-109-100-15
; Sequence 15, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: McGraw, Thomas J.
; APPLICANT: McGraw, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-15

Query Match 89.2%; Score 1108; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 3.8e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 86
Db 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 60
QY 87 KTVAGSKMOGLLERVNTETHFVTKCAFQPPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 146
Db 61 KTVAGSKMOGLLERVNTETHFVTKCAFQPPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 120
QY 147 RQNFSCLELQCPDSTLPPWSPRLEATAPOPPPLLLLLLPGVGLLLAAACWLH 206
Db 121 RQNFSCLELQCPDSTLPPWSPRLEATAPOPPPLLLLLLPGVGLLLAAACWLH 180
QY 207 WQTRRRTPRGEQVPPVSPQDLLLLVEH 235
Db 181 WQTRRRTPRGEQVPPVSPQDLLLLVEH 209

RESULT 14
US-09-109-100-13
; Sequence 13, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: McGraw, Thomas J.
; APPLICANT: McGraw, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-13

Query Match 89.1%; Score 1107; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 4.8e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 86
Db 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 60
QY 87 KTVAGSKMOGLLERVNTETHFVTKCAFQPPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 146
Db 61 KTVAGSKMOGLLERVNTETHFVTKCAFQPPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 120
QY 147 RQNFSCLELQCPDSTLPPWSPRLEATAPOPPPLLLLLLPGVGLLLAAACWLH 206
Db 121 RQNFSCLELQCPDSTLPPWSPRLEATAPOPPPLLLLLLPGVGLLLAAACWLH 180
QY 207 WQTRRRTPRGEQVPPVSPQDLLLLVEH 235
Db 181 WQTRRRTPRGEQVPPVSPQDLLLLVEH 209

RESULT 15
US-09-109-100-8
; Sequence 8, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGraw, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-8

Query Match 89.0%; Score 1106; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 6.1e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 86
Db 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 60
QY 87 KTVAGSKMOGLLERVNTETHFVTKCAFQPPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 146
Db 61 KTVAGSKMOGLLERVNTETHFVTKCAFQPPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 120
QY 147 RQNFSCLELQCPDSTLPPWSPRLEATAPOPPPLLLLLLPGVGLLLAAACWLH 206
Db 121 RQNFSCLELQCPDSTLPPWSPRLEATAPOPPPLLLLLLPGVGLLLAAACWLH 180
QY 207 WQTRRRTPRGEQVPPVSPQDLLLLVEH 235
Db 181 WQTRRRTPRGEQVPPVSPQDLLLLVEH 209

Search completed: April 1, 2002, 06:16:38
Job time: 164 sec

Mon Apr 1 06:15:15 2002

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